

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 16:30:17 ; Search time 61 Seconds
(without alignments)
1426.633 Million cell updates/sec

Title: US-09-530-209A-2

Perfect score: 1583

Sequence: 1 MAENLESLCTESNVNDE.....SACCFSPKTHDSSSYTHLS 308

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Jan04: *
1: geneseqp1980a: *
2: geneseqp1990a: *
3: geneseqp2000a: *
4: geneseqp2001a: *
5: geneseqp2002a: *
6: geneseqp2003a: *
7: geneseqp2003bs: *
8: geneseqp2004a: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1579	99.7	308	3 AAG47103	Aag47103 Arabidops
2	1573	99.4	308	2 AAY14071	Aay14071 Mitogenic
3	1565	98.9	308	3 AAG23337	Aag23337 Arabidops
4	1473	93.1	287	3 AAG47104	Aag47104 Arabidops
5	1459	92.2	287	3 AAG23338	Aag23338 Arabidops
6	1404	88.7	273	3 AAG47105	Aag47105 Arabidops
7	1390	87.8	273	3 AAG23339	Aag23339 Arabidops
8	627.5	39.6	358	7 ABR61588	Abri61588 Z. mays c
9	621.5	39.3	358	3 AAY79321	Aay79321 Maize cyc
10	620.5	39.2	358	3 AAY79322	Aay79322 Maize cyc
11	554.5	35.0	390	3 AAY79323	Aay79323 Maize cyc
12	531.5	33.6	388	2 AAY31897	Aay31897 Corn cycl
13	443.5	28.0	328	3 AAG29789	Aag29789 Arabidops
14	443.5	28.0	339	3 AAG29788	Aag29788 Arabidops
15	441.5	27.9	320	3 AAG29790	Aag29790 Arabidops
16	416.5	26.3	339	2 AAY31894	Aay31894 Soybean c
17	402	25.4	318	2 AAY31895	Aay31895 Soybean c
18	362.5	22.9	367	3 AAG23346	Aag23346 Arabidops
19	353	22.3	361	3 AAG53864	Aag53864 Arabidops
20	353	22.3	361	3 AAG07075	Aag07075 Arabidops
21	349	22.0	307	3 AAG23347	Aag23347 Arabidops
22	343.5	21.7	308	3 AAG07076	Aag07076 Arabidops
23	343.5	21.7	308	3 AAG53865	Aag53865 Arabidops
24	301.5	19.0	359	5 AAY75636	Aay75636 M. Truncu
25	294.5	18.6	238	2 AAY31892	Aay31892 Corn cycl

ALIGNMENTS

RESULT 1
AAG47103

ID AAG47103 standard; protein; 308 AA.

XX AAG47103;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SQ ID NO: 59333.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

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Matches 307; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAEENLESLCTESNVDDGMIVDTPLEIETIPQMGFSQSESEIIMEMVEKEKQHLPS 60
DB 1 MAEENLESLCTESNVDDGMIVDTPLEIETIPQMGFSQSESEIIMEMVEKEKQHLPS 60
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DB 61 DDYIKRLRSGDLDLVNRRDALNWIWKAQEVHGFGLCFCLAMNYLDRLFSVHDLPSGKG 120
QY 121 WILQLLAVACLALAAKIEETEVEPMLIDLVQVDPQFVFEAKSVORMELLVNLKWLRLAI 180
DB 121 WILQLLAVACLALAAKIEETEVEPMLIDLVQVDPQFVFEAKSVORMELLVNLKWLRLAI 180
QY 181 TPCSYIRYFLRKMCKDQPSNTLISRSLOVIASTTKGIDFLFRPSEAAAAVALSVSGE 240
DB 181 TPCSYIRYFLRKMCKDQPSNTLISRSLOVIASTTKGIDFLFRPSEAAAAVALSVSGE 240
QY 241 LQRVHFDNSSFPLFSLLOKERVKKIGEMIESDGLCSQTPNGVLEVSACCFSEFKTHDS 300
DB 241 LQRVHFDNSSFPLFSLLOKERVKKIGEMIESDGLCSQTPNGVLEVSACCFSEFKTHDS 300
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DB 301 SSSYTHLS 308

RESULT 2
AA14071
ID AA14071 standard; protein; 308 AA.
XX AA14071;
XX
XX 16-JUL-1999 (first entry)
DT Mitogenic cyclin CYCD4 protein sequence.
DE
DE Mitogenic cyclin; CYCD4; modulator; plant cell cycle; growth inhibitor;
KW plant cell division; cell growth; regulator; cell proliferation;
KW growth regulator; herbicide; cell division progression.
XX
XX Arabidopsis thaliana.
OS
XX WO9922002-A1.
PN
XX 06-MAY-1999.
PD
XX 23-OCT-1998; 98WO-EP006749.
PF
XX 24-OCT-1997; 97EP-00203303.
XX
XX (CROP-) CROPDISEGN NV.
XX
XX Inze D, De Veylder L, De Almeida J;
XX
XX WPT; 1999-312966/26.
DR
XX N-PSDB; AAX36897.
XX
XX DNA sequence encoding a mitogenic cyclin.
XX
XX Claim 1; Page 47-49; 57pp; English.
XX
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CC This sequence is the mitogenic cyclin, CYCD4, of the invention. The DNA
CC sequence, vectors containing it, protein encoded by it, or antibodies
CC recognising the protein can be used for modulating plant cell cycle,
CC plant cell division and/or growth, for influencing the activity of
CC mitogenic cyclin in a plant cell, as positive or negative regulator of
CC cell proliferation, for modifying the growth inhibition caused by
CC environmental stress conditions, or for use in a screening method for the
CC identification of inhibitors or activators of cell cycle proteins. A
CC compound which is an activator or inhibitor of the mitogenic cyclin can
CC be used as a growth regulator and/or herbicide. The proteins can also be
CC used to influence cell division progression in yeast, mammals and insects
XX
XX Sequence 308 AA;
XX
XX Query Match 99.4%; Score 1573; DB 2; Length 308;
XX Best Local Similarity 99.7%; Pred. No. 2.4e-165;
XX Matches 307; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 MAEENLESLCTESNVDDGMIVDTPLEIETIPQMGFSQSESEIIMEMVEKEKQHLPS 60
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DB 301 SSSYTHLS 308

RESULT 3
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ID AAG23337 standard; protein; 308 AA.
XX AAG23337;
XX
XX 17-OCT-2000 (first entry)
DT Arabidopsis thaliana protein fragment SEQ ID NO: 26608.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
OS
XX EP1033405-A2.
PN
XX 06-SEP-2000.
PD
XX 25-FEB-2000; 2000EP-00301439.
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XX 25-FEB-1999; 99US-0121825P.
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 26609.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX EP1033405-A2.
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Best Local Similarity 99.0%; Pred. No. 9,4e-153;
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Db 61 LNWIKACEVHQFGPICFCLAMNYLDRFLSVHDLPSGKGWILQLLAVACLSAAKTEETE 120
QY 142 VPMILIDQVGDQFVFEAKSVQRMELLVNLKWLRLRAITPCSYIRYFLKMSKCDQEPS 201
Db 121 VPMILIDQVGDQFVFEAKSVQRMELLVNLKWLRLRAITPCSYIRYFLKMSKCDQEPS 180
QY 202 NTLISRLQVIATTKGIDFLFRPSEAAAVALSVGELQRVHFDNSSFPLFSLLQKE 261
Db 181 NTLISRLQVIATTKGIDFLFRPSEAAAVALSVGELQRVHFDNSSFPLFSLLQKE 240
QY 262 RVKIKGIMIESDGLSCQTPNGVLEVSACCFKFKTHDSSSYTHLS 308
Db 241 RVKIKGIMIESDGLSCQTPNGVLEVSACCFKFKTHDSSSYTHLS 287
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RESULT 6
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XX AAG47105;
AC AAG47105;
XX 18-OCT-2000 (first entry)
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XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
XX Arabidopsis thaliana.
PN EP1033405-A2.
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DB 1 MGFSSQSESEIIMENVEKEKQHLPSDDYIKRLRSGDLNLNVRDNLNWKACEVHQFG 60
QY 96 PLCFCFLANNYLDRFLSVHDLPSGKGWILQLLAVACLSLAAKIETEVEPMLIDLQVGDPOF 155
DB 61 PLCFCFLANNYLDRFLSVHDLPSGKGWILQLLAVACLSLAAKIETEVEPMLIDLQVGDPOF 120
QY 156 VFEAKSVQRMELLVLNKLKWLRLRAITPCSYIRYFLRKMSKCDQEPSNTLISRSLQVIAS 215
DB 121 VFEAKSVQRMELLVLNKLKWLRLRAITPCSYIRYFLRKMSKCDQEPSNTLISRSLQVIAS 180
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181 TKGIDFLFRPSEAAANVALSVSGELQVHFDNSSFPLFSLLOKERVKKIGEMIESDGS 240
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AC AAG23339;
DT
XX 17-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 26610.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26610.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
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XX EP1033405-A2.
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PD 06-SEP-2000.
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PR 08-JUL-1999; 99US-0142803P.
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PR 19-JUL-1999; 99US-0144331P.
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PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 23-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
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PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.

QY 38 FSQSEEEIEMVEKEKQHLPSDDYIKRL--RSGDLNLNVRGRDALNWIWKACEVHQFG 95
 DB 64 ----LSDDCVATLVEKEVEHMPAEGYLOKQRRHGDLAAVRKDAIDWIKVIEHYNFA 119
 QY 96 PLCFCIAMNYLDRFLSVHDLPSGKGMILQLLAVACLSLAAKTEETVPMILDLQVGDPOF 155
 DB 120 PLTAVLSVNYLDRFLSTYFPEGRAMWTQLLAVACLSLASKIEETFPVPLDLQVAEAKF 179
 QY 156 VFEAKSVQRMELLVNKLKWLRAITPCSYIRYFLRMSKCDQEPSNTLISRSLOVIAS 215
 DB 180 VFEGRIRKMKELLVSTLTKRMHVAVTACSFVEFLHKLSD-HGAPSLARSRLDLVLT 238
 QY 216 TKGIDFLFRPSEAAAVALSVSGELQRVHFDNSFSLFLQKERVKKIGEMIE---- 271
 DB 239 AKGAEFVFRPSEIAASVALAIGECRSSVIERAASSCKY--LDKERVLRCHMIQEKIT 296
 QY 272 -----SDGSLCS--QTPNGVLEVSAC-----CFSFKTHDSSSS 303
 DB 297 AGSIVLKSGSSISSVPQSPIGVLDAAACLSQQSDDATVGSAPVCY----HSSSTS 348
 RESULT 9
 ID AAY79321 standard; protein; 358 AA.
 XX AAY79321;
 XX 18-JUL-2000 (first entry)
 DT Maize cyclin D.
 DE Maize; cyclin D; ZmCycD; CycD; cell division; cell cycle;
 KW transgenic plant.
 OS Zea mays.
 PN WO200017364-A2.
 PD 30-MAR-2000.
 XX 21-SEP-1999; 99WO-US021946.
 PF 23-SEP-1998; 98US-0101551P.
 PR (PION-) PIONEER HI-BRED INT INC.
 PA Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, Mcclver JA;
 PI Hoerster GJ;
 XX WPI; 2000-283589/24.
 DR N-PSDB; AA294581.
 XX Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3,
 PT related proteins and antisense RNA useful for control of cell cycle
 PT regulation.
 XX Claim 16; Page 117-118; 134pp; English.

The present sequence is that of an isoform of maize cyclin D (CycD), a
 protein necessary for progression from G1 into S phase. CycD binds to
 CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma
 associated protein, releasing the E2F transcription factor which
 activates DNA synthesis. The invention provides maize CycD
 polynucleotides (see AA294581-84) and polypeptides (see AAY79321-24) that
 are involved in cell cycle regulation. Also provided are recombinant
 expression cassettes (including ZmCycD in sense or antisense
 orientation), host cells, transgenic plants (especially corn, sorghum,
 sunflower, safflower, wheat, rice, alfalfa or oilseed brassica) and
 antibody compositions. A claimed method of modulating the level of CycD
 protein in a cell comprises transforming the cell with a recombinant
 expression cassette comprising a CycD polynucleotide linked to a
 promoter, and growing the cell for a time sufficient to induce expression

CC of the polynucleotide sufficient to modulate (increase or decrease) the
 CC CycD protein in the cell. The CycD protein is present in an amount
 CC sufficient to alter cell division, increase the number of cells dividing,
 CC improve transformation frequencies, alter cell growth, increase the
 CC growth rate, increase crop yield, alter plant height or size, enhance or
 CC inhibit organ (seed, root, shoot, ear, tassel, stalk, pollen, stamen)
 CC growth, produce organ ablation, produce parthenocarpic fruits, produce
 CC male sterile plants, enhance embryogenic response, increase callus
 CC induction, provide positive selection, increase plant regeneration, alter
 CC the time that cells are arrested in G1 or G0 phase or in a particular
 CC cell cycle, improve response to environmental stress including
 CC dehydration, heat or cold, increase the number of pods per plant,
 CC increase the number of seeds per pod or ear, alter the lag time in seed
 CC development, provide hormone-independent cell growth, or increase the
 CC growth rate of cells in bioreactors. The level of CycD protein in the
 CC cells is transiently modulated by introducing CycD RNA or CycD
 CC polypeptides. All claimed
 XX
 SQ Sequence 358 AA;

Query Match 39.3%; Score 621.5; DB 3; Length 358;
 Best Local Similarity 39.9%; Pred. No. 1e-59;
 Matches 142; Conservative 59; Mismatches 74; Indels 81; Gaps 10;
 QY 10 LLCTESN-----VDDGEM-----IVDETPTIEISIPQMG 37
 DB 12 LLCAEDNAAILGLDDDDGEESWAAATPPRTVAAAATGVAVDGILTEFPL----- 63
 QY 38 FSQSEEEIEMVEKEKQHLPSDDYIKRL--RSGDLNLNVRGRDALNWIWKACEVHQFG 95
 DB 64 ----LSDDCVATLVEKEVEHMPAEGYLOKQRRHGDLAAVRKDAIDWIKVIEHYNFA 119
 QY 96 PLCFCIAMNYLDRFLSVHDLPSGKGMILQLLAVACLSLAAKTEETVPMILDLQVGDPOF 155
 DB 120 PLTAVLSVNYLDRFLSTYFPEGRAMWTQLLAVACLSLASKIEETFPVPLDLQVAEAKF 179
 QY 156 VFEAKSVQRMELLVNKLKWLRAITPCSYIRYFLRMSKCDQEPSNTLISRSLOVIAS 215
 DB 180 VFEGRIRKMKELLVSTLTKRMHVAVTACSFVEFLHKLSD-HGAPSLARSRLDLVLT 238
 QY 216 TKGIDFLFRPSEAAAVALSVSGELQRVHFDNSFSLFLQKERVKKIGEMIE---- 271
 DB 239 AKGAEFVFRPSEIAASVALAIGECRSSVIERAASSCKY--LDKERVLRCHMIQEKIT 296
 QY 272 -----SDGSLCS--QTPNGVLEVSAC-----CFSFKTHDSSSS 303
 DB 297 AGSIVLKSGSSISSVPQSPIGVLDAAACLSQQSDDATVGSAPVCY----HSSSTS 348

RESULT 10
 ID AAY79322 standard; protein; 358 AA.
 XX AAY79322;
 XX 18-JUL-2000 (first entry)
 DT Maize cyclin D.
 DE Maize; cyclin D; ZmCycD; CycD; cell division; cell cycle;
 KW transgenic plant.
 OS Zea mays.
 PN WO200017364-A2.
 PD 30-MAR-2000.
 XX 21-SEP-1999; 99WO-US021946.
 PF 23-SEP-1998; 98US-0101551P.
 PR (PION-) PIONEER HI-BRED INT INC.

XX PI Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, Mcelver JA;
PI Hoerster GJ;
XX WPI; 2000-283589/24.
XX N-PSDB; AA294582.
XX Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3,
XX related proteins and antisense RNA useful for control of cell cycle
XX regulation.
XX Claim 16; Page 121-122; 134pp; English.
XX The present sequence is that of an isoform of maize cyclin D (CycD), a
XX protein necessary for progression from G1 into S phase. CycD binds to
XX CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma
XX associated protein, releasing the E2F transcription factor which
XX activates DNA synthesis. The invention provides maize CycD
XX polynucleotides (see AA294581-84) and polypeptides (see AAY79321-24) that
XX are involved in cell cycle regulation. Also provided are recombinant
XX expression cassettes (including ZmCycD in sense or antisense
XX orientation), host cells, transgenic plants (especially corn, sorghum,
XX sunflower, safflower, wheat, rice, alfalfa or oilseed Brassica) and
XX antibody compositions. A claimed method of modulating the level of CycD
XX protein in a cell comprises transforming the cell with a recombinant
XX expression cassette comprising a CycD polynucleotide linked to a
XX promoter, and growing the cell for a time sufficient to induce expression
XX of the polynucleotide sufficient to modulate (increase or decrease) the
XX CycD protein in the cell. The CycD protein is present in an amount
XX sufficient to alter cell division, increase the number of cells dividing,
XX improve transformation frequencies, alter cell growth, increase the
XX growth rate, increase crop yield, alter plant height or size, enhance or
XX inhibit organ (seed, root, shoot, ear, tassel, stalk, pollen, stamen)
XX growth, produce organ ablation, produce parthenocarpic fruits, produce
XX male sterile plants, enhance embryogenic response, increase callus
XX induction, provide positive selection, increase plant regeneration, alter
XX the time that cells are arrested in G1 or G0 phase or in a particular
XX cell cycle, improve response to environmental stresses including
XX dehydration, heat or cold, increase the number of pods per plant,
XX increase the number of seeds per pod or ear, alter the lag time in seed
XX development, provide hormone-independent cell growth, or increase the
XX growth rate of cells in bioreactors. The level of CycD protein in the
XX cells is transiently modulated by introducing CycD RNA or CycD
XX polypeptides. All claimed
XX Sequence 358 AA;

QY 10 LLCTSN-----VDDEGM-----IVDTTPEISIPQM 37
DB 12 LCAEDNAAILGLDDGESSWAAATPPRTVAAAATGVAVDGLTFEPL----- 63
QY 38 FQOSESEIIMBEKEKQHLPSDDYIKRL--RSGDLNVGRDRLNWKACEVHFG 95
DB 64 ----LSDCCVATLVEKEVHEMPAEGYQLQRHGDLDLVAVKQADIMWIKVIEHNP 119
QY 96 PLCFCLAMNYLDRFLSVHDLPSPGKGMILLOLLAVACLAKIETEVEPMLDLQVDPQF 155
DB 120 PLTAVLSVNYLDRFLSTVEFPEGRAWMTQLLAVACLSLAKIEETFPVPLDLQVAAKF 179
QY 156 VPEAKSVQRMELLVLNKLWRLRAITPCSYIRYFLRMSKQDQPSNTLISRLQVIAT 215
DB 180 VFEGRITKEMELLVLSTLKWHRHVAFTACSFVEYFLHLKLD-HGAPSLARSSRLVLST 238
QY 216 TKGIDFLFPRPEAAVAALSVSGELQRVHFNPSFSLFLQLQERVKKIGEMIE---- 271
DB 239 AKGAEFVFRPEIAASVALAIGECRSVIERASSCKY--LDKERVLRCHMIQEKIT 296
QY 272 -----SDGSLCS--QTPNGVLEVSAC-----CFSFKTHDSSSS 303

DB 297 MGSIVLKSAGSSISSVPOSPIGVLDAAACLSQSDDATVGSFVACY-----HSSSTS 348

RESULT 11
AAY79323
ID AAY79323 standard; protein; 390 AA.
XX
AC AAY79323;
DT 18-JUL-2000 (first entry)
XX
XX Maize cyclin D.
DE
KW Maize; cyclin D; ZmCycD; CycD; cell division; cell cycle;
KW transgenic plant.
XX
OS Zea mays.
XX
PN WO200017364-A2.
XX
PD 30-MAR-2000.
XX
PF 21-SEP-1999; 99WO-US021946.
XX
PR 23-SEP-1998; 98US-0101551P.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, Mcelver JA;
PI Hoerster GJ;
XX
XX WPI; 2000-283589/24.
DR N-PSDB; AA294583.
XX
XX Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3,
XX related proteins and antisense RNA useful for control of cell cycle
XX regulation.
XX Claim 16; Page 124-125; 134pp; English.
XX The present sequence is that of an isoform of maize cyclin D (CycD), a
XX protein necessary for progression from G1 into S phase. CycD binds to
XX CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma
XX associated protein, releasing the E2F transcription factor which
XX activates DNA synthesis. The invention provides maize CycD
XX polynucleotides (see AA294581-84) and polypeptides (see AAY79321-24) that
XX are involved in cell cycle regulation. Also provided are recombinant
XX expression cassettes (including ZmCycD in sense or antisense
XX orientation), host cells, transgenic plants (especially corn, sorghum,
XX sunflower, safflower, wheat, rice, alfalfa or oilseed Brassica) and
XX antibody compositions. A claimed method of modulating the level of CycD
XX protein in a cell comprises transforming the cell with a recombinant
XX expression cassette comprising a CycD polynucleotide linked to a
XX promoter, and growing the cell for a time sufficient to induce expression
XX of the polynucleotide sufficient to modulate (increase or decrease) the
XX CycD protein in the cell. The CycD protein is present in an amount
XX sufficient to alter cell division, increase the number of cells dividing,
XX improve transformation frequencies, alter cell growth, increase the
XX growth rate, increase crop yield, alter plant height or size, enhance or
XX inhibit organ (seed, root, shoot, ear, tassel, stalk, pollen, stamen)
XX growth, produce organ ablation, produce parthenocarpic fruits, produce
XX male sterile plants, enhance embryogenic response, increase callus
XX induction, provide positive selection, increase plant regeneration, alter
XX the time that cells are arrested in G1 or G0 phase or in a particular
XX cell cycle, improve response to environmental stresses including
XX dehydration, heat or cold, increase the number of pods per plant,
XX increase the number of seeds per pod or ear, alter the lag time in seed
XX development, provide hormone-independent cell growth, or increase the
XX growth rate of cells in bioreactors. The level of CycD protein in the
XX cells is transiently modulated by introducing CycD RNA or CycD
XX polypeptides. All claimed
XX Sequence 390 AA;

altered levels of the cyclin protein in a transformed host cell. This would have the effect of altering the regulation of cell division in those cells. The nucleic acid fragments may be used to express cyclins in plant cells to enhance cell tissue culture growth. The availability of nucleic acid sequences encoding all or a portion of cyclins should facilitate studies of cell cycle in plants, provide genetic tools to enhance cell growth in tissue culture, increase the efficiency of gene transfer and help provide more stable transformations. The proteins can be used as targets to facilitate design and/or identification of inhibitors of those enzymes that may be useful as herbicides

Sequence 388 AA;
 XX
 SQ

236	GCVGRPSETAAVA	AAVAGVD	DADGVENACCAHVD	-----KERVLRQCEAI	283
267	GEMTESDGS	DLCS	-----	-----QTPNGVLEVSACCFKTHDSSSS	303
284	GSMASAAIDATVP	PKSARRRSP	VPVPSQPVGLD	-----AAPCLISYRSEAAATA	335

AT	17-OCT-2000	(first entry)	
AD			Arabidopsis thaliana protein fragment SEQ ID NO: 35502.
DE			Protein identification; signal transduction pathway; metabolic pathway;
XX			hybridisation assay; genetic mapping; gene expression control; promoter;
KW			termination sequence.
KW			XX
XX			XX
OS			Arabidopsis thaliana.
XX			XX
PN			EP1033405-A2.
XX			XX
PD			06-SEP-2000.
XX			XX
PF			25-FEB-2000: 2000EP-00301439.

PR	29-MAR-1999;	99US-0136785P.
PR	01-APR-1999;	99US-0127462P.
PR	06-APR-1999;	99US-0128234P.
PR	08-APR-1999;	99US-0128714P.
PR	16-APR-1999;	99US-0129845P.
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PR	21-APR-1999;	99US-0130449P.
PR	23-APR-1999;	99US-0130510P.

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PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
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PR 19-JUL-1999; 99US-0144334P.
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PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
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PR 14-OCT-1999; 99US-0159637P.

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PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
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PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match      28.0%; Score 443.5; DB 3; Length 328;
Best Local Similarity 37.0%; Pred. No. 5e-40;
Matches 117; Conservative 53; Mismatches 105; Indels 41; Gaps 11;

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XX AC AAG29788;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 35501.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
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XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
XX EP1033405-A2.
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3	621.5	39.3	358	US-09-398-858-2	Sequence 2, Appli
4	620.5	39.2	358	US-09-398-858-12	Sequence 12, Appl
5	554.5	35.0	390	US-09-398-858-14	Sequence 14, Appl
6	443.5	28.0	335	US-09-404-296B-28	Sequence 28, Appl
7	440.5	27.8	315	US-09-404-296B-8	Sequence 8, Appli
8	398	25.1	376	US-09-404-296B-32	Sequence 32, Appl
9	379	23.9	373	US-09-404-296B-4	Sequence 4, Appli
10	370.5	23.4	367	US-09-404-296B-6	Sequence 6, Appli
11	357.5	22.6	357	US-09-404-296B-10	Sequence 10, Appl
12	291.5	18.4	349	US-09-398-858-22	Sequence 22, Appl
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14	237	15.0	295	US-08-464-517-20	Sequence 20, Appl
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ALIGNMENTS

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; Patent No. 6559358
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/09/404,296B
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-404-296B-2

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; Patent No. 6518487
; GENERAL INFORMATION:
; APPLICANT: Lowe, Keith S.
; APPLICANT: Tao, Yumin
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Gregory, Carolyn A.
; APPLICANT: McElver, John A.
; APPLICANT: Hoerster, George J.
; TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides
; TITLE OF INVENTION: and Methods of Use
; FILE REFERENCE: 0926
; CURRENT APPLICATION NUMBER: US/09/398,858
; CURRENT FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 60/101,551
; PRIOR FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
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; ORGANISM: Zea mays
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; CURRENT APPLICATION NUMBER: US/09/404,296B
; CURRENT FILING DATE: 1999-09-24

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; LENGTH: 335
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-404-296B-28

Query Match 28.0%; Score 443.5; DB 4; Length 335;
Best Local Similarity 37.0%; Pred. No. 1.1e-42;
Matches 117; Conservative 53; Mismatches 105; Indels 41; Gaps 11;

Qy 7 ELSLLCTESNVDDEGMIVDETPIEISIPQMGFSQSSESE-----EIMEMVEKEKQHLPSDD 62
Db 19 DMDLFCGE---DSGVFSGESTVD-----FSSEVDSWPGDSIACFIEDERHFVPGHD 67
Qy 63 YIKELRGDLDNVRDNLNWIWKAQVHGFCLFCFLAMNYLDRFLSVHDLPSGKWI 122
Db 68 YLSRFQTRSLDAS--AREDSVAMILKQAYNFQPLTAYLVNLYDRFLYARRLPETSQWP 126
Qy 123 LQLLAVACLSIAAKIETEVPMLIDLQVGDPOFVFEAKSVORMELLVNLKWLRLAITP 182
Db 127 MQLLAVACLSIAAKIETEVPMLIDLQVGDPOFVFEAKSVORMELLVNLKWLRLAITP 186
Qy 183 CSYIRYFLRKMCKCDQEPSNT---LISRSLOVIASITTKGIDFLFRPSEAAAVALSVS 238
Db 187 FDFISFYAYKI-----DPSGTFLGFFISHATEIILSNIKASFLFEPSPSSIAAAILCVA 241
Qy 239 GELQRVHFDNSFSPLFSL-----LQKERVKIGEMIES-----DGSCLCSQTPNGV--LE 287
Db 242 NELPSL---SSVNPSPHSPETWCDGLSKEKIVRCYRLMKAMAIENNL--NTPKVIKLR 296
Qy 288 VSACCFSEKTHDSSSS 303
Db 297 VSVRASSTLRPSDES 312

RESULT 7

US-09-404-296B-8
; Sequence 8, Application US/09404296B
; Patent No. 6559358
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/09/404,296B
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Helianthus tuberosus
US-09-404-296B-8

Query Match 27.8%; Score 440.5; DB 4; Length 315;
Best Local Similarity 36.6%; Pred. No. 2.3e-42;
Matches 111; Conservative 59; Mismatches 102; Indels 31; Gaps 9;

Qy 10 LLCTESNVDDEGMIVDETPIEISIPQMGFSQS--ESEEIMEMVEKEKQHLPSDDYIKRLR 68
Db 12 LLCE-----DSGILSGDDRPECS---YDFEYSGDFDSDIAEFIEQERKFVPGIDYVERFQ 64
Qy 69 SGDLNVRDNLNWIWKAQVHGFCLFCFLAMNYLDRFLSVHDLPSGKGMILQLLAV 128
Db 65 SQVLDAS--AREDSVAMILKQVRFVGFQPLTAYLVNLYDRFLYCRGFPVANGWPLQLLSV 123
Qy 129 ACSLSIAAKIETEVPMLIDLQVGDPOFVFEAKSVORMELLVNLKWLRLAITPSCVIRY 188
Db 124 ACSLSIAAKIETEVPMLIDLQVGDPOFVFEAKSVORMELLVNLKWLRLAITPSCVIRY 183
Qy 189 FLKRMKCDQEPSNT---LISRSLOVIASITTKGIDFLFRPSEAAAVALSVSGELQV 244

```
Db 184 FSHKI-----DPSGMYTGLISRATQIILNQASLLLEYWPCSTAAATILCAASDLSKF 238
QY 245 HFDNSFSPLF-SLQKERVKKIGEMIESDGLCSQTPNGV---LEVSACCFSPKTHDS 300
Db 239 SLINADHASSWCGLSKKIKTCYRLV-----QSPKILPVHVRVMTARVSTESGDS 289
QY 301 SSS 303
Db 290 SSS 292

RESULT 8
US-09-404-296B-32
; Sequence 32, Application US/09404296B
; Patent No. 6559358
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/09/404,296B
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-404-296B-32

Query Match 25.1%; Score 398; DB 4; Length 376;
Best Local Similarity 32.9%; Pred. No. 2.6e-37;
Matches 106; Conservative 58; Mismatches 96; Indels 62; Gaps 11;

QY 9 SLICTESNVDDGMIVDETP--IEISIPQMGFSQS---ESEIIMWVEKEKQHLPSDDY 63
Db 21 ALYCEEKWDDEGEVEENSLSSSSPFVLQQLFWEDEDLVTLFSKEERQGLSCLD- 79
QY 64 IKRLSGDLDLNVRDLDALNIWKAACEVHQFGLCFCLAMNYLDRFLSVHDLPSGKGWIL 123
Db 80 -----DVLSTDRKEAGWILRVNAHGFSTLAALVLAITYLDFKFCYSIQROKPMML 132
QY 124 QLLAVACLAAKIBETEYPMILDLQVGPQFVFEAKSVQRMELLVINKLWRLRAITPC 183
Db 133 QLVSVACLAAKVEETQVPLLLDFQVEETKYVFEAKTIQRMELLILSTLEWKHLITPI 192
QY 184 SVIRYFLRK-----MSKCDQEPNTLISRLQVIASITTKGIDLEFRPSEAAA 232
Db 193 SFVDHIIRLGLKNNHWDPIAKCH-----RLLSVYSDSRFVGLPSVAAA 240
QY 233 VALSVSGELQRVHFNSSP-SPLFSLIQ--KERVKKIGEMIESDGLCSQTPNGVLEVS 289
Db 241 TWMRIIEQVD--PFDPFLSYQTNLLGVNLTKKVKTC-----YDLILQLP-----VD 285
QY 290 ACCFSF-----KTHDSSSS 303
Db 286 RICLQIQSSKKRSHDSSSS 307

RESULT 9
US-09-404-296B-4
; Sequence 4, Application US/09404296B
; Patent No. 6559358
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/09/404,296B
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 373
; TYPE: PRT

; ORGANISM: Nicotiana tabacum
US-09-404-296B-4

Query Match 23.9%; Score 379; DB 4; Length 373;
Best Local Similarity 31.0%; Pred. No. 4e-35;
Matches 113; Conservative 65; Mismatches 94; Indels 92; Gaps 17;

QY 4 ENLELS-----LLCTESN-----VDEGMIVDETPI--EIS-----IQM 36
Db 7 EQQELSQSFLDLALYCEEKEEKGWLDVDDETII---TPLSSEVTTTTTTTTTKPNSLLPIL 63
QY 37 GFSQS---ESEIIMWVEKEKQHLPSDDYIKRLSGDLDLNVGRDLDALNIWKAACEVHQ 93
Db 64 LLEQDLFWEDDELLSLFSKEKETHCFWNSF-----QDSSLCSARVDSVEWILKNGVYG 118
QY 94 FGPLCFCLAMNYLDRFLSVHDLPSGKGWILQLLAVACLAAKIBETEYPMILDLQVGP 153
Db 119 PSALTAVLAINVDFRFLTSLHYQDKPWWIQLAAVTCLSLAAKVEETQVPLLLDFQVEDA 178
QY 154 QVFEAKSVQRMELLVINKLWRLRAITPCSVIRYFLRKS-----KCDQEPN 202
Db 179 KYVFEAKTIQRMELLVSLKRWMPVTPLSFLDHIIRLGLRNNIHWFLRRCB---N 234
QY 203 TLISRLQVIASITTKGIDLEFRPSEAAAVALSVSGELQ---RVHFDNSFSPLFSLIQ 259
Db 235 LLLS-----IMADCR---FVRYPMSVLATAIMLHVHQVEPCNSVDYQNLGLVL--KIN 284
QY 260 KERVKKIGEMIESDGLCSQ-----TPNGVLEVSACCFSKTH-----DS 300
Db 285 KEKVNCFELI---SEVCSKPISHKRYENPNPSHSPSGVIDP---IYSSSSNDSWDLES 337
QY 301 SSSY 304
Db 338 TSSY 341

RESULT 10
US-09-404-296B-6
; Sequence 6, Application US/09404296B
; Patent No. 6559358
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/09/404,296B
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-404-296B-6

Query Match 23.4%; Score 370.5; DB 4; Length 367;
Best Local Similarity 32.3%; Pred. No. 3.8e-34;
Matches 97; Conservative 62; Mismatches 84; Indels 57; Gaps 10;

QY 42 ESEIIMWVEKEKQHLPSDDYIKRLSGDLDLNVGRDLDALNIWKAACEVHQFGLCFCL 101
Db 58 EDDQLVTLTKKESHLGFDCLIS---DGDGFLVEVRKEALDWMLRVIAHYGFTAMTAVL 114
QY 102 AMNYLDRFLSVHDLPSGKGWILQLLAVACLAAKIBETEYPMILDLQVGPQVFEAKS 161
Db 115 AVNYDFRVSGLCFQKOKPMSQLAAVACLAAKVEETQVPLLLDLQVADSRVFEAKT 174
QY 162 VQRMELLVINKLWRLRAITPCSVIRYFLRK-----MSKCDQEPNTLISRLQ 210
Db 175 IQRMELLVSLTKWKNMPTVPLSFIDHIMRRFGFTNLLHDLFLRCR-----LI---LG 226
QY 211 VIASITTKGIDLEFRPSEAAAVALSVSGELQ---RVHFDNSFSPLFSLQKRVK-- 265
Db 227 IITDSR-----LLHYPPSVIATAVYVINEIPECNAMEYQNLMTVL-----KVQDS 275
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QY 266 -----IGEMIESDQSDLCSQ-----TPNGVLEVSACCFSKFTHDSSSYTHLS 308
Db 276 FEECHDLILELMTGSGYNICQSLKRKHQSPGSPGVIDAYFSCDS--SNDSSWSVASSIS 333

RESULT 11
US-09-404-296B-10
; Sequence 10, Application US/09404296B
; Patent No. 6559358
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/09/404,296B
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Helianthus tuberosus
US-09-404-296B-10

Query Match 22.6%; Score 357.5; DB 4; Length 357;
Best Local Similarity 31.1%; Pred. No. 1.2e-32;
Matches 101; Conservative 65; Mismatches 114; Indels 45; Gaps 12

QY 9 SLCTES-----NVDD--GMIVDETPEI-SIPQMGFSQSESEIIMEMVEKQ 56
Db 14 TLFNEQODHYHEYEBDEFTQTTLTSSDLHLPPLQDLDSWEHELVSUFTKEQSQ 73
QY 57 -HLPSSDDYIKRLRSGDLLNV--GRRDALNIWKACEVHQFGPLCFCLAMNYLDRFLSVH 113
Db 74 KQTPC----TLSTGKTSPSVFAARKEAVDMILKVKSCYGVFTPLTALAINYDRFLSSL 128
QY 114 DLPGKGWILQLLAVACLSLAAKIBETEVPMILDIQGDGPOFVFAKSVQRMELLVLNKL 173
Db 129 HFQEDKPWMIQLVAVSCLSLAAKVBETQVPLLLDQVEDTKYLFEAKNIQKMELLVMSTL 188
QY 174 KWRRLAIPCSYIRYFLRKMSKCDPEPNTLISRSLOVIATSTKCIDFLFEPSEAAAV 233
Db 189 KWRNWPVTPISFLDHIVARLGLTDHVWD-FPKKCEAMILCLVSDSRFCYKPSVLATAT 247
QY 234 ALSVSGELQRVHFNDSFSPFLSLQ--KERVKKTIGEMI-----ESDGDSDLCSQ 280
Db 248 MLHVVEIDPPNCIDYK-SQLDLLKTKTKDDINECYELIVELAYDHNKXKHDANETTIN 306
QY 281 --TPNGVLEVSACCFSKFTHDSSSS 303
Db 307 PVSPAGVIDE-----TCDESSN 323

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; SEQ ID NO 22
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Zea mays
US-09-398-858-22

Query Match      18.4%; Score 291.5; DB 4; Length 349;
Best Local Similarity 31.1%; Pred. No. 5.1e-25;
Matches 75; Conservative 43; Mismatches 96; Indels 27; Gaps 5

Qy   10 LLCTESNVD-----DEGMIVDETPIEISIPOMGFSQSSESIIMEMVKEKHQH-----L 58
    | :|: |||||
Db   18 LILCEDGSLLADADGA--GTDLVAVARDERLLWDDDEYVALLLSKESASGGGPVE 74
    | :|: |||||
Qy   59 PSDIYIKLRSGDLDLVNGRRDALNTWKACEVHQFGPLCFCLAMNYLDRLFVHDLPSG 118
    | :|: |||||
Db   75 EMEDWMKAARSQ-----CVRWIKTTFAMPFRFGKTAAYAVNYLDRLAQRRVRE 124
    | :|: |||||
Qy   119 KGWTQLQLLAACLSLAAKIETEPEMLIDLQVGPPQFVFEEKSVORMELLVLNKLKWLRLR 178
    | :|: |||||
Db   125 HANGQLQLLVACMSLATKLEEHAPRLSELFLDACEFAFDRAVLRMELLVLGTLEWRMV 184
    | :|: |||||
Qy   179 AITPCSVIRVFLRKMSCKDQSPSNTLSRSLOVTASTTKGIDFLEFRSEAAAAAVALSVS 238
    | :|: |||||
Db   185 AVTPFPYISCAAFR---QDERRAVLVRAVECVPFAAIRAMSSVEYQPSTTAVASILVAR 241
    | :|: |||||
Qy   239 G 239
Db   242 G 242

RESULT 13
US-08-770-761A-2
; Sequence 2, Application US/08770761A
; Patent No. 5814503
; GENERAL INFORMATION:
; APPLICANT: Kovacevic, Steven
; APPLICANT: Otto, Keith A.
; TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE
; TITLE OF INVENTION: REGULATORY PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Division
; CITY: Indianapolis
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,761A
; FILING DATE: 19-DEC-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10136
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-376-0756
; TELEFAX: 317-277-1917
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 660 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-770-761A-2
```

Query Match 15.1%; Score 239.5; DB 2; Length 660;
Best Local Similarity 28.5%; Pred. No. 1.5e-18;
Matches 88; Conservative 51; Mismatches 115; Indels 55; Gaps 14;
US-08-464-517-20

Query Match 15.0%; Score 237; DB 2; Length 295;
Best Local Similarity 28.4%; Pred. No. 8.1e-19;
Matches 83; Conservative 52; Mismatches 115; Indels 42; Gaps 13;
US-08-464-517-20

QY 1 MAERN-----LRLSLLCTESNVDDGMIWDETPPIISIPQMGFSQSESEIIME 49
DB 15 MAEQKLISEEDLLAMEHQLLCCEV-----ET-IRRAYPDANLL---NDRVLR 60

QY 50 MVEKEKQLPSDDYIKRLRSGDLNVGRDALNWKACEVHQFGLCFCLAMNYLDRF 109
DB 61 MKRAEETCAPSVSYFKVQKEVLPDM--RKIVATWMLVECBQCEBEVFLPAMNYLDRF 118

QY 110 LSVHDLPSGKGWILQLLAVACLSLAAKIEETEVPMLIDLQVDPQFVFEAKSVQ-----R 164
DB 119 LSLPEVKKSR---LQLLGATCMFVASKMKET-IPL-----TAEKLCIYTDNSIRPEELLQ 169

QY 165 MELLVNLKWLRLRAITPCSYIRYFLRKMSKCDQPSNTLISRSLOV-IASITTKGIDFLE 223
DB 170 MELLVNLKWLRLRAITPCSYIRYFLRKMSKCDQPSNTLISRSLOV-IASITTKGIDFLE 227

QY 224 FRPS-EAAAVALSVSGELQRFVHFDNSGFSPLFSLQKERVKKIGEMIESDGSLL--CSQ 280
DB 228 NPPSWVAGSVAAVQGLNLR-----SPNNFLSYRLTRFLSRVVKCDPDCLRAQOE 279

QY 281 TPNGVLEVS 289
DB 280 QIEALLESS 288

RESULT 14
US-08-464-517-20
; Sequence 20, Application US/08464517
; Patent No. 5869640
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,517
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,514
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew P. Vincent
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-004C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 295 amino acids
; TYPE: amino acid

RESULT 15
US-08-246-361A-20
; Sequence 20, Application US/08246361A
; Patent No. 5998582
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/246,361A
; FILING DATE: 19-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,514
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew P. Vincent
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-004C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 295 amino acids
; TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-517-20

Query Match 15.0%; Score 237; DB 2; Length 295;
Best Local Similarity 28.4%; Pred. No. 8.1e-19;
Matches 83; Conservative 52; Mismatches 115; Indels 42; Gaps 13;
US-08-464-517-20

QY 6 LELSLCTESNVDDGMIWDETPPIISIPQMGFSQSESEIIMEVMEKQHLPSDDYIK 65
DB 1 MENQLLCCV-----ET-IRRAYPDANLL---NDRVLRAMLKTEETCAPSVSYFK 46

QY 66 RLRSGLDLNVGRDALNWKACEVHQFGLCFCLAMNYLDRFSLVHDLPSGKGWILQL 125
DB 47 CVQKEIVPSM--RKIVATWMLVECBQCEBEVFLPAMNYLDRFSLVHDLPSGKGWILQL 101

QY 126 LAVACLSLAAKIEETEVPMLIDLQVDPQFVFEAKSVQ-----RMELLVNLKWLRLRAI 180
DB 102 LGATCMFVASKMKET-IPL-----TAEKLCIYTDNSIRPEELLQWELLVNLKWLRLRAI 155

QY 181 TPCSYIRYFLRKMSKCDQPSNTLISRSLOV-IASITTKGIDFLEFRPSEAAAAVALSVSG 239
DB 156 TPDFIEHFLSKMP--DAEENKQIIRKHAQTFFALCATDVKFISNPFMSVAAG---SMVA 210

QY 240 ELQRFVHFDNSGFSPLFSLQKERVKKIGEMIESDGSLL--CSQTPNGVLEVS 289
DB 211 AMQGLNLG-----SPNNFLSYRYTRTHFLSRVVKCDPDCLRAQOEALLESS 258

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-246-361A-20

Query Match 15.0%; Score 237; DB 2; Length 295;
Best Local Similarity 28.4%; Pred. No. 8.1e-19;
Matches 83; Conservative 52; Mismatches 115; Indels 42; Gaps 13;
Qy 6 LELSLCTESNVDEGMIVDETPTEISIPQMGFSQSEETIMEMVEKEKQHLPSDDYIK 65
Db 1 MENQLLCEV-----ET-IRRAYPTNLI-----NDRVIRAMKTEETCAPSVSYFK 46
Qy 66 RLRSGLDLNVRDRDALNWIWKACEVHQFGPLCFCLAMNYLDRLFSVHDLPSGKGWILQL 125
Db 47 CVQKEIVPSM--RKIVATWMLEVCEEQCEEEVFLAMNYLDRLFSLEPLKSR---LQL 101
Qy 126 LAVACLSLAAKIEETEVPMLIDLQVDDQGFVFEAKSVQ-----RMELLVLNKLKRLRAI 180
Db 102 LGATCMFVASMKET-IPL-----TAELKIYTDNISIRPEELLQWELLVNLKKNLAAM 155
Qy 181 TPCSVIRYFLRKMSKCDQEPSNTLISRSLOV-IASSTKGIDFLFRPSEAAAAVALSVSG 239
Db 156 TPHEFIEHFLSKMP--DAENKQIRKHAQTFVALCATDVKFINPFSMWVAG---SMVA 210
Qy 240 ELQRVHFDNSSFPLFLSLQKERVKKIGEMIESDGSGL--CSQTPNGVLEVS 289
Db 211 AMQGLNLG----SPNNFLSRVYRTHFLSRVIKCDPCLCLACQEQIEALLESS 258

Search completed: March 23, 2004, 16:40:15
Job time : 24 secs

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OM protein - protein search, using sw model

Run on: March 23, 2004, 16:39:06 ; Search time 50 Seconds
(without alignments)

1595.165 Million cell updates/sec

Title: US-09-530-209A-2

Perfect score: 1583

Sequence: 1 MAENLELSLLCTESNVDDDE.....SACCFKTHDSSSYTHLS 308

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	722.5	45.6	354	15	US-10-388-269-2
2	627.5	39.6	358	15	US-10-409-701-5
3	621.5	39.3	358	14	US-10-320-230-2
4	620.5	39.2	358	14	US-10-320-230-12
5	613.5	38.8	323	12	US-10-425-114-38749
6	595	37.6	345	12	US-10-425-114-53407
7	595	37.6	345	12	US-10-425-114-56939
8	585.5	37.0	340	12	US-10-425-114-49308
9	563.5	35.6	344	15	US-10-310-154-411
10	554.5	35.0	390	14	US-10-320-230-14
11	521.5	32.9	356	15	US-10-310-154-430
12	501	31.6	251	12	US-10-424-599-273602
13	486	30.7	229	12	US-10-424-599-226651
14	480	30.3	309	12	US-10-424-599-218205
15	477.5	30.2	238	12	US-10-424-599-273603

16	440.5	27.8	315	15	US-10-388-269-8
17	416.5	26.3	351	12	US-10-424-599-187989
18	416.5	26.3	383	12	US-10-425-114-53864
19	416.5	26.3	389	12	US-10-425-114-37533
20	413.5	26.1	321	15	US-10-310-154-422
21	410	25.9	182	12	US-10-424-599-239678
22	410	25.9	271	12	US-10-424-599-235479
23	379	23.9	373	15	US-10-388-269-4
24	370.5	23.4	367	15	US-10-388-269-6
25	365	23.1	383	12	US-10-424-599-160824
26	365	23.1	427	12	US-10-425-114-38905
27	364.5	23.0	371	12	US-10-424-599-160823
28	364.5	23.0	394	12	US-10-425-114-48711
29	357.5	22.6	357	15	US-10-388-269-10
30	347.5	22.0	362	12	US-10-424-599-178575
31	326.5	20.6	316	12	US-10-424-599-213831
32	325	20.3	349	12	US-10-424-599-178576
33	322	20.3	383	12	US-10-424-599-282528
34	314.5	19.9	305	12	US-10-424-599-169546
35	306	19.3	129	12	US-10-424-599-250717
36	301	19.0	255	12	US-10-424-599-171019
37	291.5	18.4	349	14	US-10-320-230-22
38	287.5	18.2	349	15	US-10-310-154-423
39	275.5	17.4	390	12	US-10-425-114-37564
40	259.5	16.4	387	15	US-10-310-154-421
41	257	16.2	349	15	US-10-310-154-428
42	247.5	15.6	391	15	US-10-310-154-425
43	247	15.6	349	15	US-10-310-154-426
44	241	15.2	289	13	US-10-024-066-2
45	237	15.0	185	12	US-10-424-599-221849

ALIGNMENTS

RESULT 1

US-10-388-269-2

; Sequence 2, Application US/10388269

; Publication No. US2003022121A1

; GENERAL INFORMATION:

; APPLICANT: MURRAY, James Augustus Henry

; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH

; FILE REFERENCE: 2121-0151P

; CURRENT APPLICATION NUMBER: US/10/388,269

; CURRENT FILING DATE: 2003-03-12

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 2

; LENGTH: 354

; TYPE: PRT

; ORGANISM: Nicotiana tabacum

US-10-388-269-2

Query Match 45.6%; Score 722.5; DB 15; Length 354;

Best Local Similarity 48.1%; Pred. No. 2.5e-67;

Matches 164; Conservative 60; Mismatches 76; Indels 41; Gaps 10;

Qy	1	MAENLELSLLCTESNV	-----DDEGMIVDETPTETISIPQMGFSQ-----S	41
Db	1	MAADNYDFVASULLCTETKSLCFDDVDSLTISQONITKSKDLSFNNGTRSEPLDLP	60	
Qy	42	ESSEIEMWVEKSKOHLPSDDYIKRLRSGLDNLNVRDRLNWKACEVHQFGPLCFCL	101	
Db	61	LSECLSPWQREMEFLPKDDYVERLRSGDLDSV-RKEALDWLKAHHYGFGLSFL	119	
Qy	102	AMNYLDRFLSVHDLPSGKGWILQLLAVACLSLAKEETEVPMLIDLQVGDPOFVFEAK	161	
Db	120	SINYLDRLFLSVLPSRKTWTQVLLAVACLSLAKEEINNVPLTVDLQVGDPRFVEGKT	179	
Qy	162	VORMELLVINKLWRLRAITPCSYIRFLKMKSCDOEPNLTISRSLQVIASTTKGIDF	221	
Db	180	IQRMELLVLTWKRMQATPYTFIDYFMKNG-DQIPRPLISGSMQILSIIRSIDF	238	

Matches	142;	Conservative	59;	Mismatches	74;	Indels	81;	Gaps	10
QY	10	LLCTESN-----VDDEGM-----							IVDETPIEISIPQM 37
Db	12	LLCAEDNAAILGLDDGEESSWAAAAATPPRDTVAATAATGAVVDGILTEPFL							63
QY	38	FSQSEEEIIMEMVEKEKOHLPDDDYIKRL--RSGDLDLNVGRDNLNWIWKACEVHQF 95							
Db	64	----LSDDCVATLVEKEVEHMPAEGYLOKQRRHGDDLDLVAVRKDAIDWIWKVIEHNF 119							
QY	96	PLFCFLAMNYLDRFLSPGKGWTLQLLAACLSLAAKIEETVPMPLDLQVGDPQF 155							
Db	120	PLTAVLSVNYLDRFLSYEPPEGRAWWTQLLAACLSLASKIEETFPFLDLQVAEAKF 179							
QY	156	VFAKSVORMELLVNLKWLRLRAITPCSYIRYFLRKMSCKDQPSNTLISRSLOVIAS 215							
Db	180	VFEGRITKRMELLVSLTKWRMHAVTACSFVEYFLHKLSD--HGAPSLAARSSDLVLST 238							
QY	216	TKGIDFLFPPRPEAAAAVALSVSGELQVRHVDNSFSFLFLLOKERVKKIGEMIE--- 271							
Db	239	AKGAEFVVPFSELAASVALAAIGCRSSVIERAASSCKY--LDKERVLRCHEMIOEKIT 296							
QY	272	-----SDGSDLCs--QTPNGVLEVSAC-----CFSPKTHDSSS 303							
Db	297	MGSIVLKSGAGSISGVPSPGIVLDAACLSQSSDDATVGSFAVCY---HSSSTS 348							
RESULT 5									
US-10-425-114-38749									
; Sequence 38749, Application US/10425114									
; Publication No. US20040034888A1									
; GENERAL INFORMATION:									
; APPLICANT: Liu, Jingdong									
; APPLICANT: Zhou, Yihua									
; APPLICANT: Kovalic, David K.									
; APPLICANT: Screen, Steven E.									
; APPLICANT: Tabaska, Jack E.									
; APPLICANT: Cao, Yongwei									
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated W									
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement									
; FILE REFERENCE: 38-21(531313)B									
; CURRENT APPLICATION NUMBER: US/10/425,114									
; CURRENT FILING DATE: 2003-04-28									
; NUMBER OF SEQ ID NOS: 73128									
; SEQ ID NO 38749									
; LENGTH: 323									
; TYPE: PRT									
; ORGANISM: Zea mays									
; FEATURE:									
; OTHER INFORMATION: Clone ID: UC-ZMFLB73363C10_FLI.pgp									
US-10-425-114-38749									
Query Match 38.8%; Score 613.5; DB 12; Length 323;									
Best Local Similarity 45.0%; Pred. No. 7.1e-56;									
Matches 131; Conservative 55; Mismatches 68; Indels 37; Gaps 7									
QY	43	SEEIIMEMVEKEKOHLPDDDYIKRL--RSGDLDLNVGRDNLNWIWKACEVHQFGLCFC 100							
Db	30	SDDCVATLVEKEVEHMPAEGYLOKQRRHGDDLDLAAVRKDAIDWIWKVIEHNFAPLTAV 89							
QY	101	LAMNYLDRFLSPGKGWTLQLLAACLSLAAKIEETVPMPLDLQVGDPQFVFEAK 160							
Db	90	LSVNYLDRFLSYEPPEGRAWWTQLLAACLSLASKIEETFPFLDLQVAEAKFVEGR 149							
QY	161	SVORMELLVNLKWLRLRAITPCSYIRYFLRKMSCKDQPSNTLISRSLOVIAS 220							
Db	150	TTKRMELLVSLTKWRMHAVTACSFVEYFLHKLSD--HGAPSLAARSSDLVLSTAKGAE 208							
QY	221	FLEFPPEAAAAVALSVSGELQVRHVDNSFSFLFLLOKERVKKIGEMIE----- 271							
Db	209	FVVFPRSELAASVALAAIGCRSSVIERAASSCKY--LDKERVLRCHEMIOEKITAGSIV 266							
QY	272	--SDGSDLCs--QTPNGVLEVSAC-----CFSPKTHDSSS 303							


```
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-310-154-430

Query Match      32.9%; Score 521.5; DB 15; Length 356;
Best Local Similarity 44.4%; Pred. No. 4.2e-46;
Matches 119; Conservative 49; Mismatches 89; Indels 11; Gaps 6;

QY 42 ESEETIWEVEKEKQHLPSDDYIKRLRSGLDLNVGRDNLNWKACEVHGFPLCFCL 101
Db 60 DSEDFVALLVEKEMHQPGYGLKLELGLGEC-SWKDAIDWICKVHYHFGPLSLYL 118
QY 102 AMNYLDRFLSVHDLPSGKGWILQLLAVACLSLAAKIEETEVEPMLIDLQVGDQPQVFEAKS 161
Db 119 AVNYLDRFLSSFNPLPHDESMMQQLSVCSLSLATKMEETVWPLPMDLQVFDABYFEARH 178
QY 162 VQMEILLVNLKWLRLRAITPCSYIRYFLKMSKCDQEPSNTILSRSLQVIASITTKGIDF 221
Db 179 IKEMELIVMKTLLKWLRLQAVTPFSFIGYFLDKFNE-GKPPSYTLASWCSDLTGVTLKDSRF 237
QY 222 LEPRPSEAAAVALSVSGELORVHFONSPSPFLSLLOKERVKKIGE-MIES-----DG 274
Db 238 LSPRPSEIAAAVVLAEVQFLV-NSALGESEIPVNMKEMWRCYELMVEKALVKIRN 296
QY 275 SDCSQTPNGVLEV-SACCFSEFKTHDS 301
Db 297 SNASSVPHSPITVLDAACFSPRSDDTT 324

RESULT 12
US-10-424-599-273602
; Sequence 273602, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 273602
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Glycine max
; NAME/KEY: unsure
; LOCATION: (1)..(251)
; FEATURE:
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_89084C.1.pep
US-10-424-599-273602

Query Match      31.6%; Score 501; DB 12; Length 251;
Best Local Similarity 44.7%; Pred. No. 3.7e-44;
Matches 119; Conservative 43; Mismatches 58; Indels 46; Gaps 7;

QY 55 KQHLPSDDYIKRLRSGLDLNVGRDNLNWKACEVHGFPLCFCLAMNYLDRFLSVHD 114
Db 7 EENLPQDGYLKRLLSGDLDSV-RKEALDWTK----- 38
QY 115 LPSGKGWILQLLAVACLSLAAKIEETEVEPMLIDLQVGDQPQVFEAKSVQRMELLVNLKJ 174
Db 39 --RGSWSMQLAVACLSIAAAMEIKVPPCVDLQVLPKFAFKDIQRMELLVLTSLR 96
QY 175 WRLRAITPCSYIRYFLKMSKCDQEPSNTILSRSLQVIASITTKGIDFLEFRPSEAAA 234
Db 97 WKMQASFPFLDYFLAKIT-CDQIVKSSILRSVGPLNLIKCNFLFRPSEIAA 155

; LENGTH: 356
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-310-154-430

Query Match      32.9%; Score 521.5; DB 15; Length 356;
Best Local Similarity 44.4%; Pred. No. 4.2e-46;
Matches 119; Conservative 49; Mismatches 89; Indels 11; Gaps 6;

QY 42 ESEETIWEVEKEKQHLPSDDYIKRLRSGLDLNVGRDNLNWKACEVHGFPLCFCL 101
Db 60 DSEDFVALLVEKEMHQPGYGLKLELGLGEC-SWKDAIDWICKVHYHFGPLSLYL 118
QY 102 AMNYLDRFLSVHDLPSGKGWILQLLAVACLSLAAKIEETEVEPMLIDLQVGDQPQVFEAKS 161
Db 119 AVNYLDRFLSSFNPLPHDESMMQQLSVCSLSLATKMEETVWPLPMDLQVFDABYFEARH 178
QY 162 VQMEILLVNLKWLRLRAITPCSYIRYFLKMSKCDQEPSNTILSRSLQVIASITTKGIDF 221
Db 179 IKEMELIVMKTLLKWLRLQAVTPFSFIGYFLDKFNE-GKPPSYTLASWCSDLTGVTLKDSRF 237
QY 222 LEPRPSEAAAVALSVSGELORVHFONSPSPFLSLLOKERVKKIGE-MIES-----DG 274
Db 238 LSPRPSEIAAAVVLAEVQFLV-NSALGESEIPVNMKEMWRCYELMVEKALVKIRN 296
QY 275 SDCSQTPNGVLEV-SACCFSEFKTHDS 301
Db 297 SNASSVPHSPITVLDAACFSPRSDDTT 324

RESULT 13
US-10-424-599-226651
; Sequence 226651, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 226651
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Glycine max
; NAME/KEY: unsure
; LOCATION: (1)..(229)
; FEATURE:
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_46697C.1.pep
US-10-424-599-226651

Query Match      30.7%; Score 486; DB 12; Length 229;
Best Local Similarity 47.2%; Pred. No. 1.2e-42;
Matches 102; Conservative 36; Mismatches 46; Indels 32; Gaps 5;

QY 9 SLLCTESNVDDSGMIVDETPI-----SIFDENDYGSVEVLEDAWQDPYRRNLSQSENLDPN-GWFLQSD 63
Db 10 SLLCVEDN-----SIFDENDYGSVEVLEDAWQDPYRRNLSQSENLDPN-GWFLQSD 63
QY 45 EIMEMVEKEKQHLPSDDYIKRLRSGLDLNVGRDNLNWKACEVHGFPLCFCLAMN 104
Db 64 ECLRLMVEKEWDHLPNGDYRNKLSRGLDLE-ARKEAIDMIQVQEHFGFVPCAYLSIN 122
QY 105 YLDRFLSVHDLPSGKGWILQLLAVACLSLAAKIEETEVEPMLIDLQVGDQPQVFEAKSVOR 164
Db 123 YLDRFLSVAYELPKHRTWTWQLAVGCLSLAAKMEETDAPMSLDLQVGESKYIFEAKTOR 182
QY 165 MELLVNLKWLRLRAITPCSYIRYFLKMSKCDQEP 200
Db 183 MELLVNLTLRWRMQAITPXSFDIDHFLYKIND-DQSP 217

RESULT 14
US-10-424-599-218205
; Sequence 218205, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 218205
```

Job time : 58 secs

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; LENGTH: 309
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_39067C.1.pep
US-10-424-599-218205

Query Match      30.3%; Score 480; DB 12; Length 309;
Best Local Similarity 41.5%; Pred. No. 8.2e-42;
Matches 110; Conservative 44; Mismatches 83; Indels 28; Gaps 7;

Qy 44 EEIIMVVEKEKQHLPSDDYIKRLSRGDLNNGRRDALNWIWKAACEVHOFGLCFCLAM 103
Db 20 EAATAGLLDPEHPMPKDYLRRCRDSVDV-TARLDVAVWILKVHAYEFPVTAFLSV 78

Qy 104 NYLDRFLSVHDLF--SGKGWTLQLLAVACLAAKIEETEVPMLIDIQVGDPQPVFEAKS 161
Db 79 NYDFRFLSRCSLPQSG-GWAFQLSVACLAAKMEESHVPFLDLQLFEPKVFPEPKT 137

Qy 162 VORMELLVLNKLKWLRAITPCSVIRYFLRXM-SKCDQEPSNTLISRSLQVIASITTKGID 220
Db 138 IQRMELWMSNLKWLRSVTPFDYLRHVFISKLPSSSSQSLNHHFFSTSSNLILSTTRVIN 197

Qy 221 FLEFRPSE-AAAAVAALSVSGELQVRHFDNSSFPLFSLQKERVYKIGEMIESDGLC- 278
Db 198 FLGAPSTVAAAVLCSANGQLPLSFHD-----IRDEMVRCCQMLMEYVVDTCP 248

Qy 279 -----SOTPNGVLEVSAC 291
Db 249 ASIKVRITEAAAPSSPVGVLDATC 273

RESULT 15
US-10-424-599-273603
; Sequence 273603, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 273603
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_89085C.1.pep
US-10-424-599-273603

Query Match      30.2%; Score 477.5; DB 12; Length 238;
Best Local Similarity 58.6%; Pred. No. 1e-41;
Matches 92; Conservative 30; Mismatches 28; Indels 7; Gaps 3;

Qy 42 ESEIIMVVEKEKQHLPSDDYIKRLSRGDLNNGRRDALNWIWKAACEVHOFGLCFCL 101
Db 89 QSDETVGLVGRSEHLPVGVYKRLSLGDLDSV-RKEALDWIWKAHAYDFGPGCSLCL 147

Qy 102 AMNYLDRFLSVHDLFSGKGWTLQLLAVACLAAKIEETEVPMLIDIQVGDPQPVFEAKS 161
Db 148 SVNLYDRFLSVYELPRGKSWNQMLLAVACLSTAAKMEIYKVPCCVDL-----QFAFEAKD 202

Qy 162 VORMELLVLNKLKWLRAITPCSVIRYFLRXM-SKCDQ 198
Db 203 IQRMELLVLSTURMKWQASTFDFLDFRKIT-CDQ 238
```

Search completed: March 23, 2004, 16:45:20

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 16:35:16 ; Search time 26 Seconds
(without alignments)
1139.500 Million cell updates/sec

Title: US-09-530-209A-2

Perfect score: 1583

Sequence: 1 MAENLELSLLCTSNVDDE.....SACCFSPKTHDSSSYTHLS 308

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	954	60.3	317	T49995	cyclin protein-lik
2	650.5	41.7	372	T09961	cyclin D-like prot
3	635.5	40.1	361	C84613	probable cyclin D
4	633	40.0	383	S51651	cyclin delta-2 - A
5	443.5	28.0	339	A96725	hypothetical prote
6	434	27.4	334	S51650	cyclin delta-1 - A
7	392	24.8	376	T05420	cyclin delta-3 - A
8	354.5	22.4	386	T09598	cyclin 4, D-type -
9	353	22.3	361	T45860	cyclin D3-like pro
10	305	19.3	302	B5041	probable D-type cy
11	285.5	16.8	321	T04720	hypothetical prote
12	260.5	16.5	291	S57922	cyclin D1 - Africa
13	253	16.0	291	S62730	cyclin D1 - zebra
14	242	15.3	288	T58372	cyclin D2 - rat
15	241	15.2	289	A41984	cyclin D2 - mouse
16	239	15.1	295	A56523	cyclin D1 - mouse
17	236	14.9	295	A38977	cyclin D1 - human
18	235	14.8	295	JC2342	cyclin D1 - rat
19	232	14.7	289	A42822	cyclin D2 - human
20	231	14.6	288	JC4011	cyclin D2 - rat
21	224.5	14.2	291	JC4579	cyclin D2 - chicke
22	220.5	13.9	291	S57925	cyclin D2 - Africa
23	216.5	13.7	502	T02746	cyclin A-like prote
24	204.5	12.9	456	C57742	cyclin II - maize
25	198	12.5	454	A96803	probable mitotic c
26	188.5	11.9	395	A40270	cyclin E - human
27	187.5	11.8	493	T03609	cyclin, A-type - c
28	181.5	11.5	482	T02967	cyclin A-type (clo
29	181	11.4	292	B42822	cyclin D3 - human

30 180.5 11.4 483 2 T02966 cyclin A-type (clo
31 180.5 11.4 483 2 T03606 cyclin, A-type - c
32 175.5 11.1 426 2 S17792 cyclin A - common
33 174.5 11.0 341 2 T48232 hypothetical prote
34 173 10.9 293 2 JC4012 cyclin D3 - rat
35 171 10.8 428 2 S56679 mitosis-specific c
36 171 10.8 460 2 P96505 probable mitotic c
37 170.5 10.8 372 2 T09982 cyclin A-type - Ma
38 170 10.7 348 2 T07669 cyclin ai-type, mi
39 170 10.7 484 2 T07675 cyclin a2-type, mi
40 168.5 10.6 406 2 S24788 cyclin A - bovine
41 167.5 10.6 314 2 T02964 cyclin A-type (clo
42 167.5 10.6 432 2 S08277 cyclin A - human
43 167 10.5 328 2 S29925 cyclin 2 - alfalfa
44 167 10.5 380 2 S64417 cyclin B6 - yeast
45 166 10.5 425 2 S53004 mitosis-specific c

ALIGNMENTS

RESULT 1

T49995

cyclin protein-like - Arabidopsis thaliana

N:Alternate names: protein F12B17.210

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

C:Accession: T49995

R:Bayan, M.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.

A:Reference number: 225026

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-317 <BEV>

A:Cross-references: EMBL:AL353995; GSPDB:GN00063; ATSP:F12B17.210

A:Experimental source: cultivar Columbia; BAC clone F12B17

C:Genetics:

A:Gene: ATSP:F12B17.210

A:Map position: 5

A:Introns: 78/3; 107/3; 140/3; 221/3; 266/3

Query Match 60.3%; Score 954; DB 2; Length 317;
Best Local Similarity 64.8%; Pred. No. 1.7e-74;
Matches 212; Conservative 23; Mismatches 58; Indels 34; Gaps 8;
Qy 4 ENLESLLLCTESNVDDREGMIVDETPIBISIPQMGFSQSESEIIMENVEKEKQHLPSDDY 63
Db 3 EFNEPNLV---SNFDDEKSNVDTR---SIFQMGF-PLSESEIVREMIEXERQHSRPRDY 55
Qy 64 IKRLSGDLDLVGRRDALNWIWKAQVHQPGLCFCLANNYLDRFLSVHDLPSGKGWIL 123
Db 56 LKRLNGDLDFNV-RIQALGWIKACEELQFGLPICLANNYLDRFLSVHDLPSGKAWT 114
Qy 124 QLLAVACLSLAAKTEETEVEPMLIDLVGDPQFVFPEAKSVORMELLVNLKWLRLAITPC 183
Db 115 QLLAVACLSLAAKTEENVEFELMQLQVGAFFVFPEAKSVORMELLVNLVLRRLAIVPC 174
Qy 184 SYIRYLRKMSKCDQEPSNTLISRSLQVIATTK-----GIDFLEF 224
Db 175 SYVRYFLSKINGVDQEPHSRLVTRSLQVIATTKGDRGLGFFFGVLIVDVWAGIDFLEF 234
Qy 225 RPEAAAVALSVELQORVHFDNSFSLFLLQKRVKKGIGEMTESDGLCSQTPNG 284
Db 235 RASEIAAAVALSVSGE---HFDKFSFSSFSLEKERVKKIGEMIERDGGSSSSSSQTPNN 290
Qy 285 -VLEVSACCF--SFKTHDSSSYTHLS 308
Db 291 TVLQPKSRRYSHSLSTASVSLSLS 317

RESULT 2

T09961

cyclin D-like protein - red goosefoot
 C:Species: *Chenopodium rubrum* (red goosefoot)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C:Accession: T09961
 R:Renz, A.; Fountain, M.; Beck, E.
 submitted to the EMBL Data Library, December 1996
 A:Description: Nucleotide sequence of a cDNA encoding a D-type cyclin from a photoautotrophic source: 7 day old culture; photoautotrophic cells derived from hypocotyl
 A:Accession: T09961
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-372 <REN>
 A:Cross-references: EMBL:Y10162; NID:e1014005; PID:e290219
 A:Experimental source: 7 day old culture; photoautotrophic cells derived from hypocotyl
 C:Genetics:
 A:Gene: cyclD
 C:Keywords: cell cycle control; cell division control

Query Match 41.7%; Score 660.5; DB 2; Length 372;
 Best Local Similarity 44.1%; Pred. No. 4.1e-49;
 Matches 150; Conservative 63; Mismatches 76; Indels 51; Gaps 10;

QY 10 LLCTESN-----VDDEGM-IVDETPIEISIPQM----- 36
 DB 7 LLCAEDNSIPDEVDDNYGVDDVVLQICNLQOQHGNLNPDDFTLLILLIIKEHNFEA 66

QY 37 ---GFSQSESEIIMEMVEKEKQHLPSDDYIKRLSGDLNLNVRDRLNLTWKAQCEVHQ 93
 DB 67 LISGFFVA-NHECLASLFDNERQHLGLDYLKRFNGDLDLG-ARNLVLDTHKVKQSHYN 124

QY 94 FGPLCFCLAMNYDLRFLSVHDLPSGKGWTLQALLAVACLSLAAKIEETEVPMLIDLVQVDP 153
 DB 125 FGPLCVLVSNTLDRLFLSAIEPLP-GKAMMQLGQVACLSLAAKVDLPLLDLQVSES 183

QY 154 QVFFAKSVQRMELLVNKLKWLRAITPCSYIRYFLKMKSCDQEPNTLISRLQVIA 213
 DB 184 KVFPEAKTIQRMELLVSLTKWRMSQVTPFSDIFLYKLSG-DKMPKSLIFQAIQIL 242

QY 214 STTKGIDFLFPPSAAVAALVSVELQVRFHFNSSPSPLSLQKRVKIGEMI--- 270
 DB 243 STIKGIDLMEFRPSEIAAAVAISVTOQTQIVFTDKAFSLTDHVEKERLAKVCBIMHDL 302

QY 271 ---RSDG---SDLCSTQPNGLVSVACCFSPKTHDSSS 303
 DB 303 RMSRSNGALASTVPQSPIGVLDASA-CLSYKSDTSTT 341

RESULT 3
 C84613
 Probable cyclin D [imported] - Arabidopsis thaliana
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: C84613
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A:Reference number: AB4420; MUID:20083487; PMID:10617197
 A:Accession: C84613
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-361 <STO>
 A:Cross-references: GB:AE002093; NID:g4544444; PID:NAD22352.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g2490
 A:Map position: 2

Query Match 40.1%; Score 635.5; DB 2; Length 361;
 Best Local Similarity 42.8%; Pred. No. 5.7e-47;
 Matches 154; Conservative 58; Mismatches 75; Indels 73; Gaps 12;

QY 1 MAENLELSLCTESNVDDGMIIVDETPIEI-----SI 33

DB 1 MAE-----NLACGETS-----ESWIINDDDDDINYGCGFTNEIDYHQLFAKDNFGNGSI 52
 QY 34 PQMGFSQSE-SEETIMEMVEKEKQHLPSDDYIKRLSGDLNLNVRDRLNLTWKAQCEVH 92
 DB 53 PMWGSSSSLSLSEDIKEMLVREIFPCGTDVVKLLSGDLDSV-RNQALDWILKVCAYH 111
 QY 93 QFGPLCFCLAMNYDLRFLSVHDLPSGKGWTLQALLAVACLSLAAKIEETEVPMLIDLVQVDP 152
 DB 112 HFHGLCICLSMNYDLRFLSVYELPKDWAQAQLLAVSCLSLASKMEETDVPHIVDLQVED 171
 QY 153 PQVFFPEAKSVQRMELLVNKLKWLRAITPCSYIRYFLKMKSCDQEPNTLISRLQV 212
 DB 172 PKVFEAKTIQRMELLVSLTKWRMSQVTPFSDIFLYKLSG---GHVSENLIRSRFI 228
 QY 213 ASTTKGIDFLFPPSE-AAAVALSVSGELQVRFHFNSSPSPLSLQKRVKIGEMI 270
 DB 229 LNTTKAIEFLDFRPFSEIAAAVAALSVSISGETECIDEEKALSSLIY--VKQERVKRCNLNM 286
 QY 271 ES-----DGSDLCSQ-----TPNGVLVSVACCFSPK-----THDSSS 303
 DB 287 RSLTGEENVRGTSLSQEQARVAVRASPVGYLE--ATCLSYRSEERTVESCTNSQSS 344

RESULT 4
 S51651
 cyclin delta-2 - Arabidopsis thaliana
 N:Alternate names: cyclin D homolog
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 25-Apr-1997
 C:Accession: S51651
 R:Soni, R.; Carmichael, J.P.; Shah, Z.H.; Murray, J.A.H.
 submitted to the EMBL Data Library, December 1994
 A:Description: A family of cyclin D homologs from plants differentially controlled by g
 A:Reference number: S51650
 A:Accession: S51651
 A:Molecule type: mRNA
 A:Residues: 1-383 <SON>
 A:Cross-references: EMBL:X83370
 C:Keywords: cell cycle control; cell division control

Query Match 40.0%; Score 633; DB 2; Length 383;
 Best Local Similarity 47.7%; Pred. No. 1e-46;
 Matches 144; Conservative 53; Mismatches 67; Indels 38; Gaps 9;

QY 32 SIPQMGFSQSE-SEETIMEMVEKEKQHLPSDDYIKRLSGDLNLNVRDRLNLTWKAQCE 90
 DB 51 SIPMGSSSSLSLSEDIKEMLVREIFPCGTDVVKLLSGDLDSV-RNQALDWILKVCAY 109

QY 91 VHQFGPLCFCLAMNYDLRFLSVHDLPSGKGWTLQALLAVACLSLAAKIEETEVPMLIDLVQV 150
 DB 110 HYHFGHLCICLSMNYDLRFLSVYELPKDWAQAQLLAVSCLSLASKMEETDVPHIVDLQV 169

QY 151 GDPQVFFPEAKSVQRMELLVNKLKWLRAITPCSYIRYFLKMKSCDQEPNTLISRLQ 210
 DB 170 EDPKVPPEAKTIKEMLVVTLNWLQALTPFSDIFLYKLSG---GHVSENLIRSR 226

QY 211 VIATTKGIDFLFPPSP-AAAVALSVSGELQVRFHFNSSPSPLSLQKRVKIGEMI 268
 DB 227 FILNTTKAIEFLDFRPFSEIAAAVAALSVSISGETECIDEEKALSSLIY--VKQERVKRCNL 284

QY 269 MIES-----DGSDLCSQ-----TPNGVLVSVACCFSPK-----THDSS 301
 DB 285 LMRSLTGEENVRGTSLSQEQARVAVRASPVGYLE--ATCLSYRSEERTVESCTNSQ 342

QY 302 SS 303
 DB 343 SS 344

RESULT 5
 A96725
 hypothetical protein F20P5.7 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: A96725
 R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huijzer, L.; Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maity, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: A96725
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-339 <STO>
 A:Cross-references: GB:AE005173; NID:g2194121; PID:RAB61096.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F20P5.7
 A:Map position: 1

Query Match 28.0%; Score 443.5; DB 2; Length 339;
 Best Local Similarity 37.0%; Pred. No. 1.8e-30;
 Matches 117; Conservative 53; Mismatches 105; Indels 41; Gaps 11;

```

QY 7 ELSLCTESNVDDGMIYDETPIEIISIPQMGFSQSESE-----EIMEMVEKEKQHLPSDD 62
   :::::::::::::::::::::
DB 19 DMDLFCGE-----DSGVFSGESTVD-----FSSSEVDSWPGDSIACFTIEDERHFVPGHD 67
   :::::::::::::::::::::
QY 63 YIKLRSGDLDLVNVRDGLNWKACEVHGFQPLCFCLAMNYLDRFLSVHDLPSGKGWI 122
   :::::::::::::::::::::
DB 68 YLSRFQTRSLDAS-AREDSVAMILKVQAYNFQPLSLAYLVNMDRFLYARRLPETSGWP 126
   :::::::::::::::::::::
QY 123 LQLLAVACLSLAAKIETEVEPMLIDLVQGDQPFQVFEAKSVQRMELLVNLKWLRAITP 182
   :::::::::::::::::::::
DB 127 MQLLAVACLSLAAKMEIILVPSLFDQVAGVKYLFKAIKRMELLVNLKWLRAITP 186
   :::::::::::::::::::::
QY 183 CSYIRYFLRMKSKCDQEPSNTLISRSLOVIATTTKGIIDFLRPRSEAAAAVALSVS 238
   :::::::::::::::::::::
DB 187 FDFISFFAYKI-----DPSGTFLGFFISHATEIILSNIKESFLEYWPSIIAAAILCVA 241
   :::::::::::::::::::::
QY 239 GEIQRVHFDNSSFPLFSL-----LQKERVKKIGEMIES-----DGSDLCSQTPNGV--LE 287
   :::::::::::::::::::::
DB 242 NELPSSL---SSVNPHPESPETWCDGLSKEKIVRCYRLMKAMAIENNRL--NTPKVIATKLR 296
   :::::::::::::::::::::
QY 288 VSACCFSFKTHDSSSS 303
   :::::::::::::::::::::
DB 297 VSVRASSTLTPRSDS 312
   :::::::::::::::::::::

```

RESULT 6

S51650
 cyclin delta-1 - Arabidopsis thaliana
 N:Alternate names: cyclin D homolog
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Sep-1997
 C:Accession: S51650
 R:Soni, R.; Carmichael, J.P.; Shah, Z.H.; Murray, J.A.H.
 A:Description: A family of cyclin D homologs from plants differentially controlled by 9
 A:Reference number: S51650
 A:Accession: S51650
 A:Molecule type: mRNA
 A:Residues: 1-334 <SON>
 A:Cross-references: EMBL:X83369; NID:g603504; PID:g603505
 C:Keywords: cell cycle control; cell division control

Query Match 27.4%; Score 434; DB 2; Length 334;
 Best Local Similarity 37.2%; Pred. No. 1.2e-29;
 Matches 116; Conservative 52; Mismatches 110; Indels 34; Gaps 10;

```

QY 7 ELSLCTESNVDDGMIYDETPIEIISIPQMGFSQSESE-----EIMEMVEKEKQHLPSDD 62
   :::::::::::::::::::::
DB 19 DMDLFCGE-----DSGVFSGESTVD-----FSSSEVDSWPGDSIACFTIEDERTVPGHD 67
   :::::::::::::::::::::
QY 63 YIKLRSGDLDLVNVRDGLNWKACEVHGFQPLCFCLAMNYLDRFLSVHDLPSGKGWI 122
   :::::::::::::::::::::
DB 68 YLSRFQTRSLDAS-AREDSVAMILKVQAYNFQPLSLAYLVNMDRFLYARRLPETSGWP 126
   :::::::::::::::::::::
QY 123 LQLLAVACLSLAAKIETEVEPMLIDLVQGDQPFQVFEAKSVQRMELLVNLKWLRAITP 182
   :::::::::::::::::::::
DB 127 MQLLAVACLSLAAKMEIILVPSLFDQVAGVKYLFKAIKRMELLVNLKWLRAITP 186
   :::::::::::::::::::::
QY 183 CSYIRYFLRMKSKCDQEPSNTLISRSLOVIATTTKGIIDFLRPRSEAAAAVALSVS 242
   :::::::::::::::::::::
DB 187 FDFISFFAYKI-----DPSGTFLGFFISHATEIILSNIKESFLEYWPSIIAAAILCVA 244
   :::::::::::::::::::::
QY 243 RVHFDNSSFPLFSL-----LQKERVKKIGEMIES-----DGSDLCSQTPNGV--LEVSAC 291
   :::::::::::::::::::::
DB 245 SL---SSVNPHPESPETWCDGLSKEKIVRCYRLMKAMAIENNRL--NTPKVIATKLRVSVR 299
   :::::::::::::::::::::
QY 292 CFSFKTHDSSSS 303
   :::::::::::::::::::::
DB 300 ASSTLTTPRSDS 311
   :::::::::::::::::::::

```

RESULT 7

T05420
 cyclin delta-3 - Arabidopsis thaliana
 N:Alternate names: cyclin D homolog; protein F28A23.80
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
 C:Accession: T05420; S51652
 R:Bevan, M.; Weichechelgarnier, M.; Partmann, B.; Granderath, K.; Dauner, D.; Herzl, A.; submitted to the Protein Sequence Database, October 1998
 A:Reference number: Z15415
 A:Accession: T05420
 A:Molecule type: DNA
 A:Residues: 1-376 <BEV>
 A:Cross-references: EMBL:AL021961
 A:Experimental source: cultivar Columbia; BAC clone F28A23
 R:Soni, R.; Carmichael, J.P.; Shah, Z.H.; Murray, J.A.H.
 A:Description: A family of cyclin D homologs from plants differentially controlled by 9
 A:Reference number: S51650
 A:Accession: S51652
 A:Molecule type: mRNA
 A:Residues: 1-287,'C',289-370,'R',372-376 <SON>
 A:Cross-references: EMBL:X83371; NID:g603508; PID:g603509
 C:Genetics:
 A:Map position: 4
 A:Introns: 158/3; 226/1; 269/3
 A:Note: F28A23.80
 C:Keywords: cell cycle control; cell division control

Query Match 24.8%; Score 392; DB 2; Length 376;
 Best Local Similarity 31.9%; Pred. No. 5.6e-26;
 Matches 104; Conservative 60; Mismatches 92; Indels 70; Gaps 10;

```

QY 9 SLCTESNVDDGMIYDETP--IBISIPQMGFSQS---ESEIIMEMVEKEKQHLPSDDY 63
   :::::::::::::::::::::
DB 21 ALYCEBEKWDDEGEVEENSLSLSSSSPFVLQQLDFWEDEDLVLTFSEEQGLSCLD-- 79
   :::::::::::::::::::::
QY 64 IKELRSGDLDLVNVRDGLNWKACEVHGFQPLCFCLAMNYLDRFLSVHDLPSGKGWI 123
   :::::::::::::::::::::
DB 80 -----DVLSTDRKEAVGILRVNNAHYGFSTLAALVLAITYLDKFCISYQDRKFWML 132
   :::::::::::::::::::::
QY 124 LQLLAVACLSLAAKIETEVEPMLIDLVQGDQPFQVFEAKSVQRMELLVNLKWLRAITP 183
   :::::::::::::::::::::
DB 133 QLVSVAACLSLAAKVEETQVPLLDLFQVEETKYVFEAKTIQRMELLVNLKWLRAITP 192
   :::::::::::::::::::::
QY 184 SYIRYFLRK-----MSKCDQEPSNTLISRSLOVIATTTKGIIDFLRPRSEAAAA 232
   :::::::::::::::::::::
DB 193 SPVDHIIRRLGLKNNAHMDFLNKCH-----RLLLSVISDSRFVGLPSVAAA 240
   :::::::::::::::::::::

```



```

RESULT 12
S57922
cyclin D1 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 16-Jul-1999
C;Accession: S57922
R;Cockerill, M.J.; Hunt, T.
submitted to the EMBL Data Library, July 1995
A;Description: D-type cyclins in Xenopus laevis.
A;Reference number: S57922
A;Accession: S57922
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-291 <COC>
A;Cross-references: EMBL:X89475; NID:g897818; PIDN:CAA61664.1; PID:g897819
C;Superfamily: cyclin
C;Keywords: cell cycle control

Query Match 16.5%; Score 260.5; DB 2; Length 291;
Best Local Similarity 29.6%; Pred. No. 8.6e-15;

```

RESULT	14
I58372	
cyclin D2	

Search completed: March 23, 2004, 16:39:40
Job time : 27 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 23, 2004, 16:31:10 ; Search time 18 seconds
(without alignments)
890.978 Million cell updates/sec

Title: US-09-530-209A-2

Perfect score: 1583

Sequence: 1 MAENLELSLLCTESNVDE.....SACCFKTHDSSSYTHLS 308

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	635.5	40.1	361	1	CGD2_ARATH
2	443.5	28.0	335	1	CGD1_ARATH
3	398	25.1	376	1	CGD3_ARATH
4	260.5	16.5	291	1	CGD1_XENLA
5	253	16.0	291	1	CGD1_BRARE
6	244.5	15.4	292	1	CGD1_CHICK
7	242	15.3	288	1	CGD2_RAT
8	241	15.2	289	1	CGD2_MOUSE
9	239	15.1	295	1	CGD1_MOUSE
10	236	14.9	295	1	CGD1_HUMAN
11	235	14.8	295	1	CGD1_RAT
12	232	14.7	289	1	CGD2_HUMAN
13	224.5	14.2	291	1	CGD2_CHICK
14	220.5	13.9	291	1	CGD2_XENLA
15	188.5	11.9	410	1	CGE1_HUMAN
16	182	11.5	404	1	CGE2_HUMAN
17	181	11.4	292	1	CGE3_HUMAN
18	176	11.1	404	1	CGE2_MOUSE
19	175.5	11.1	426	1	CG2A_PATVU
20	173	10.9	292	1	CGD3_MOUSE
21	173	10.9	293	1	CGD3_RAT
22	172.5	10.9	421	1	CGA1_MOUSE
23	171	10.8	428	1	CG1B_MEDVA
24	170	10.7	465	1	CGA1_HUMAN
25	169.5	10.7	396	1	CGE1_RAT
26	168.5	10.6	406	1	CGA2_BOVIN
27	167	10.6	432	1	CGA2_HUMAN
28	167	10.5	328	1	CG2B_MEDSA
29	167	10.5	380	1	CGS6_YEAST
30	165.5	10.5	408	1	CGE1_XENLA
31	165.5	10.5	408	1	CGE2_XENLA
32	164.5	10.4	422	1	CGA2_MOUSE
33	164	10.4	410	1	CG1E_BRARE

34 163.5 10.3 421 1 CGA2_MEDAU
35 163 10.3 434 1 CG2B_MEDVA
36 163 10.3 491 1 CGE1_MOUSE
37 160.5 10.1 491 1 CG2A_DROME
38 159.5 10.1 399 1 CGB2_CHICK
39 159.5 10.1 420 1 CG2A_CHLVR
40 158.5 10.0 408 1 CGE3_XENLA
41 157.5 9.9 392 1 CGB2_RANJA
42 156.5 9.9 418 1 CGA1_XENLA
43 155.5 9.8 395 1 CGA2_CHICK
44 155.5 9.8 419 1 CG2B_ORYSA
45 153.5 9.7 407 1 CGE1_CHICK

ALIGNMENTS

RESULT 1

CGD2_ARATH
ID CGD2_ARATH STANDARD; PRT; 361 AA.
AC P42752;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cyclin delta-2.
GN CYCD2 OR AT2G22490 OR F14M13.11.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta; TISSUE=Seedling;
RX MEDLINE=95210930; PubMed=7696881;
RA Soni R., Carmichael J.P., Shah Z.H., Murray J.A.H.;
RT "A family of cyclin D homologs from plants differentially controlled
by growth regulators and containing the conserved retinoblastoma
protein interaction motif";
RL Plant Cell 7:85-103(1995).
RN [2]
RP REVISIONS.
RA Murray J.A.H.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana";
RL Nature 402:761-768(1999).
CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; X83370; CAA58286.1; --
CC EMBL; AC006592; AAD22352.1; --
CC PIR; C84613; C84613.
CC InterPro; IPR006670; Cyclin.

```

DR InterPro; IPR004367; Cyclin Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin_1.
DR SMART; SM00984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cyclin; Cell cycle; Cell division; Multigene family.
SQ SEQUENCE 361 AA; 40579 MW; 6D6DDC7673108D2F CRC64;

Query Match      40.1%; Score 635.5; DB 1; Length 361;
Best Local Similarity 42.8%; Pred. No. 4.2e-46;
Matches 154; Conservative 58; Mismatches 75; Indels 73; Gaps 12;

QY 1 MAENLESLCTENVDDEGMIVDETPIEI-----SI 33
DB 1 MAE-----NLACGTS---ESWIIDNDDDINYGCGTNEIDYNHQLFAKDNFGNGSI 52

QY 34 POMGFSQSB-SEETIMEMVEKEKQLPSDDYIKRLSRGDLNNGRRDALNIWKACEVH 92
DB 34 POMGSSSSLSDEKEMLEVRIEFCPGDYVYKRLSLGDLDSV-RNQALDWILKVCARY 111

QY 93 QFGPLCFCLAMNYLDRFLSVHDLPSGKGIQLLAVACLSLAAKIEETEVPMLIDLQVGD 152
DB 112 HFGHLCICLSMNYLDRFLSVHDLPSGKGIQLLAVACLSLAAKIEETEVPMLIDLQVGD 171

QY 153 PQVFEAKSVQRMELLVNLKWLRLAETPCSYIRYFLAKMKSCDOEPSNTLISRLQVI 212
DB 172 PKFVFEAKTIKMEILLVNTLNRQLALTFPFIDYFDVKIS---GHVSENLIYRSSRI 228

QY 213 ASTTKGIDFLFRPSE-AAAAVALSVSGELQKRVHFDNSFSFLSLQKRVKIGEMI 270
DB 229 LNTTKAIEFLDRPSEIAAAVASVISGETECIDEKALSLLIY--VKQERVKCLNLM 286

QY 271 ES-----DGSDLCSQ-----TPNGVLEVSACCFSK-----THDSGSS 303
DB 287 RSLTGENVRGTSLSQEQARVAVRAPSPVGVLE--ATCLSYRSEBRTVSCNTSQSS 344

RESULT 2
CGDI ARATH
ID CGDI ARATH STANDARD; PRT; 335 AA.
AC P42751; O04525;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cyclin delta-1.
GN CYCD1 OR AT1G70210 OR F20P5.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCB_TaxID=3702;
PI [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta; TISSUE=Seedling;
RX MEDLINE=95210930; PubMed=7696881;
RA Soni R., Carmichael J.P., Shah Z.H., Murray J.A.H.;
RT "A family of cyclin D homologs from plants differentially controlled
RT by growth regulators and containing the conserved retinoblastoma
RT protein interaction motif."
RL Plant Cell 7:85-103 (1995).
RN [2]
RP REVISIONS.
RA Murray J.A.H.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altieri J., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway T.H., Dewar K.,

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RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani A.,
RA Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana."
RL Nature 408:816-820 (2000).
CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X83369; CAA58285.1; -.
DR EMBL; AC002062; AAB61096.1; -.
DR PIR; A96725; A96725.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
DR Cyclin; Cell cycle; Cell division; Multigene family.
FT CONFLICT 313 313 S -> SFSSS (IN REF. 3).
SQ SEQUENCE 335 AA; 37868 MW; D365767F3D2FC639 CRC64;

Query Match      28.0%; Score 443.5; DB 1; Length 335;
Best Local Similarity 37.0%; Pred. No. 5.6e-30;
Matches 117; Conservative 53; Mismatches 105; Indels 41; Gaps 11;

QY 7 ELSLICTESNVDDGMIYDETPIEISIPQMGSQSESE-----EIMEMVVEKEKQLPSDD 62
DB 19 DMDLFCGE-----DSGVFSGESTVD-----FSSSEVDSPGDSIACIEDERHFVPGHD 67

QY 63 YIKRLSRGDLNNGRRDALNIWKACEVHFGPLCFCLAMNYLDRFLSVHDLPSGKGI 122
DB 68 YLSRFQTRSLDAS-AREDSVAWLKVQAVYVNPQLTAVLVNMDRFLYARRLPETSGWP 126

QY 123 LQLLAVACLSLAAKIEETEVPMLIDLQVGDQPFVEAKSVQRMELLVNLKWLRLAETP 182
DB 127 MQLLAVACLSLAAKIEETEVPMLIDLQVGDQPFVEAKSVQRMELLVNLKWLRLAETP 186

QY 183 CSYIRYFLRKMSKCDQEPSNT-----LISRLQVIASSTTKGIDFLFRPSEAAAAVALSVS 238
DB 187 PFIFISFFAYKI-----DFSGTFLGFIISHATEILLNKEASFLEYWSSIAAAILCVA 241

QY 239 GELQRVHFDNSFSFLFSL-----LQKERVKKIGEMIES-----DGSDLCSQTPNGV--LE 287
DB 242 NELPSL--SSVNPHEPSPETWCDCGLSKEKIVRCYRLMKAMAIENNL--NTPKVIATKL 296

QY 288 VSACCFSPKTHDSGSS 303
DB 297 VSVRASSTLTRESDES 312

RESULT 3
CGDI ARATH
ID CGDI ARATH STANDARD; PRT; 376 AA.
AC P42753; O49489;
DT 01-NOV-1995 (Rel. 32, Created)

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DT. 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cyclin delta-3.
 GN CYCD3 OR AT4G34160 OR F28A23.80.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsie.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Landsberg erecta; TISSUE=Seedling;
 RX MEDLINE=95210930; PubMed=7696881;
 RA Soni R., Carmichael J.P., Shah Z.H., Murray J.A.H.;
 RT "A family of cyclin D homologs from plants differentially controlled
 by growth regulators and containing the conserved retinoblastoma
 protein interaction motif.";
 RL Plant Cell 7:85-103(1995).
 RN [2]
 RP REVISION TO 371.
 RA Murray J.A.H.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
 RA Harris B., Ansgore W., Brant P., Grivell L.A., Rieger M.,
 RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
 RA Kreis M., Delgany M., Puigdomenech P., Watson M., Schmidheini T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hohnel J., Zimmermann W., Wedler H., Kidley P.,
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
 RA Van der Schueren J., Grymoprez B., Chuang Y.-J., Vandenbussche F.,
 RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Weitzenecker T., Bothe G., Ransperger U., Hilbert H., Braun M.,
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
 RA Moeljan P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
 RA Berner S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
 RA Gabel C., Fuchs M., Partmann B., Granderath K., Dauner D., Herzl A.,
 RA Neumann S., Argitoni A., Vitale D., Liguori R., Piravandi E.,
 RA Massenet O., Quigley F., Clabaud G., Muendlein A., Felber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Chafador F., Cooke R., Berger C., Montfort A., Casacuberta E.,
 RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
 RA Perez-Perez A., Furnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bieleke C.,
 RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Oedha N., Gnoj L., Schütz K., Huang E., Spiegel L.,
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
 RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antonou B., Zidanic M., Strong C., Sun H., Lanar B., Yordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
 RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
 RA Chen E., Maria M.A., Martensen R., McCombie W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 thaliana.";
 RL Nature 402:769-777(1999).
 CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.

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DR EMBL; X83371; CAA58287.1; -
 DR EMBL; AL021961; CAA17556.1; -
 DR EMBL; AL161584; CAB80133.1; -
 DR PIR; T05420; T05420.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR004367; Cyclin Cterm.
 DR Pfam; PF00134; cyclin; 1.
 DR Pfam; PF02984; cyclin C; 1.
 DR SMART; SM00385; CYCLIN; 2.
 DR PROSITE; PS00292; CYCLINS; 1.
 KW Cyclin; Cell cycle; Cell division; Multigene family.
 FT CONFLICT 288 C -> G (IN REF. 3).
 SQ SEQUENCE 376 AA; 42747 MW; FB8DSB6BC435FAC2 CRC64;

Query Match 25.1%; Score 398; DB 1; Length 376;
 Best Local Similarity 32.9%; Pred. NO. 4.4e-26;
 Matches 106; Conservative 58; Mismatches 96; Indels 62; Gaps 11;

QY 9 SLTCTESVDDGIMVDSTP--ISIPQMGFSOS---ESBEIEMWVEKSKHLPSSDY 63
 DB 21 ALYCEEKWDDEGEVENSSLSSSSSFFVVLQDLFWEDDLVTLFSEHEQGLSCLD--79
 QY 64 IKRLRSGDLNNGRRDALNINWACEVHQFGPLCFCLAMNYLDRFLSVHDLPSGKGWIL 123
 DB 80 -----DVLSTDRKEAVGILRWNAHYGFSTLAAVLATYLDKFCISYSLQRDKPWWL 132
 QY 124 QLLAVACLSIAAKTEETVEPMLIDLVCDPQVFEAKSVQRMELLVNLKWLRAITPC 183
 DB 133 QLVSVACLSIAAKVEETQVPLLDFOVEETKYVFEAKTIQRMELLTSTLEWKHLLITPI 192
 QY 184 SYIRFYLRK-----MSKCDQSPNTLSRSLOQVIASTTKGIDFLFRPSEAAA 232
 DB 193 SFVDHIIRLLKKNNAHWDFLNKCH-----RLLSVISDSRFVGYLSVVA 240
 QY 233 VALSVGELQKRVHFDNSSF-SPLFSLIQ--KERVKIGEMIESDGLCSQTPNGVLEVS 289
 DB 241 TMRRIIEQVD--PEPLSYQNLGLVNLNLTKEVKTC-----YDLILQLP-----VD 285
 QY 290 ACCFSF-----KTHDSSSS 303
 DB 286 RICLQIQISKKRKHSHSSSS 307

RESULT 4
 CGDI_XENLA
 ID CGDI_XENLA STANDARD; PRT; 291 AA.
 AC P50755;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE G1/S-specific cyclin D1.
 GN CCND1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cockerill M.J., Hunt T.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Essential for the control of the cell cycle at the G1/S
 (start) transition.

DR GO: 0016538; F: cyclin-dependent protein kinase, intrinsic . . .; IDA.
 DR GO: 0045444; P: adipocyte differentiation; IDA.
 DR GO: 0000320; P: re-entry into mitotic cell cycle; IDA.
 DR InterPro: IPR006670; Cyclin.
 DR InterPro: IPR004367; Cyclin Cterm.
 DR InterPro: IPR006671; Cyclin N.
 DR Pfam: PF00134; cyclin; 1.
 DR Pfam: PF02984; cyclin; 2.
 DR SMART: SM00385; CYCLIN; 1.
 DR PROSITE: PS00292; CYCLINS; 1.
 DR CYCLIN; Cell cycle; Cell division; Multigene family.
 KW Cyclin; Cell cycle; Cell division; Multigene family.
 SQ SEQUENCE 295 AA; 33428 MW; 3A79736B4163251B CRC64;

Query Match 15.1%; Score 239; DB 1; Length 295;
 Best Local Similarity 28.5%; Pred. No. 7.9e-13;
 Matches 83; Conservative 50; Mismatches 118; Indels 40; Gaps 12;

Qy 6 LEALLCTESNVDDGIMVDETPTEISIPQMGFSQSEEEIIMWVEKEKHLPDDYIK 65
 Db 1 MEHQLLCEV-----ET-IRAYPDNLL---NDRVLRANLKYETECAFSVYFK 46

Qy 66 RLRSGLDLNVGRDALNWIWKAQEVHQFGLCPCLANNYLDRFLSVHDPGSGKWILQL 125
 Db 47 CVQKEIVPSM--RKIVATWMLVEVCEBQCEVEVPLANNYLDRFLSVLEPLKSR---LQL 101

Qy 126 LAVACLISAAKIEETEVPMLDLQVGDPQFVFEAKSVQ-----RMELLVNLKLRRAI 180
 Db 102 LGATCMFVASKKET-IPL-----TAEKLCITYTNSIRPELLOMELLVNLKRWLAAM 155

Qy 181 TPCSYIRYFLKMSKCDQEPSNTLISLQVIASTTKGIDFLFRPSEAAAVALSVSGE 240
 Db 156 TPDDFIEHLSKMEAD-ENKQTKRKAQTVFALCATDVKFIENPPSWAAG---SVAA 211

Qy 241 LQRVHFNSFSPLFSLQKRVKIGEMIESDGSGL--CSQTPNGVLEVS 289
 Db 212 MQGLNLG----SPNNFLSCYRTTHFLSRVIRKCDPLCRACQEQIEALLSS 258

RESULT 10
 CGDI_HUMAN
 ID CGDI_HUMAN STANDARD; PRT; 295 AA.
 AC P24385;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE G1/S-specific cyclin D1 (PRAD1 oncogene) (BCL-1 oncogene).
 GN CCND1 OR PRAD1 OR BCL1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=91194766; PubMed=1826542;
 RA Motokura T., Bloom T., Kim H.G., Jueppner H., Ruderman J.V.,
 RA Kronenberg H.M., Arnold A.;
 RT "A novel cyclin encoded by a bcl1-linked candidate oncogene.";
 RN Nature 350:512-515 (1991).
 [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=91194766; PubMed=1826542;
 RA Motokura T., Bloom T., Kim H.G., Jueppner H., Ruderman J.V.,
 RA Kronenberg H.M., Arnold A.;
 RT "Isolation of three novel human cyclins by rescue of G1 cyclin (Cln)
 function in yeast";
 RN Cell 66:1197-1206 (1991).
 [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=91235304; PubMed=1827756;
 RA Xiong Y., Connolly T., Fletcher B., Beach D.;
 RT "Human D-type cyclin";
 RN Cell 65:691-699 (1991).
 [4]
 RN SEQUENCE FROM N.A.

RA MEDLINE=92017758; PubMed=1833629;
 RA Withers D.A., Harvey R.C., Faust J.B., Melnyk O., Carey K.,
 RA Meeker T.C.;
 RT "Characterization of a candidate bcl-1 gene";
 RN Mol. Cell. Biol. 11:4846-4853 (1991).
 [5]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=94264323; PubMed=8204893;
 RA Rimokh R., Berger F., Bastard C., Klein B., French M., Archimbaud E.,
 RA Rouault J.-P., Santa Lucia B., Duret L., Vuillaume M.;
 RT "Rearrangement of CCND1 (BCL1/PRAD1) 3' untranslated region in
 RT mantle-cell lymphomas and t(11q13)-associated leukemias";
 RN Blood 83:3689-3696 (1994).
 [6]
 RN SEQUENCE FROM N.A.
 RP Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Wittrak L.A., Nickerson D.A.;
 RT Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 [7]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Brain, and Placenta;
 MEDLINE=22398257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [8]
 RN INTERACTION WITH CDK4 AND CDK6.
 RX MEDLINE=94134440; PubMed=8302605;
 RA Bates S., Bonetta L., McAllan D., Parry D., Holder A., Dickson C.,
 RA Peters G.;
 RT "CDK6 (PUS7) and CDK4 (PSK-J3) are a distinct subset of the
 RT cyclin-dependent kinases that associate with cyclin D1";
 RN Oncogene 9:71-79 (1994).
 CC -/- FUNCTION: Essential for the control of the cell cycle at the G1/S
 CC (start) transition.
 CC -/- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
 CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
 CC imparts substrate specificity to the complex.
 CC -/- DISEASE: Involved in B-lymphocytic malignancy (particularly
 CC mantle-cell lymphoma (MCL)) by a chromosomal translocation
 CC t(11;14)(q13;q32) that involves CCND1 and immunoglobulin gene
 CC regions (BCL1 oncogene). Activation of CCND1 may be oncogenic by
 CC directly altering progression through the cell cycle.
 CC -/- DISEASE: Involved in a subset of parathyroid adenomas by a
 CC chromosomal translocation t(11;11)(q13;p15) that involves CCND1
 CC and the parathyroid hormone (PTH) enhancer (PRAD1 oncogene).
 CC -/- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
 CC -/- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/BCL1.html".

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DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE GI/S-specific cyclin D2.
 GN CCND2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92347851; PubMed=1386336;
 RA Xiong Y., Menninger J., Beach D., Ward D.C.;
 RT "Molecular cloning and chromosomal mapping of CCND genes encoding
 RT human D-type cyclins.";
 RL Genomics 13:575-584(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93205384; PubMed=8455931;
 RA Palmero I., Holder A., Sinclair A.J., Dickson C., Peters G.;
 RT "Cyclins D1 and D2 are differentially expressed in human B-lymphoid
 RT cell lines.";
 RL Oncogene 8:1049-1054(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Miyajima N.;
 RL Submitted (MAR-1993) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Spaplen M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lottolano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE OF 1-240 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=92347850; PubMed=1386335;
 RA Inaba T., Matsushima H., Valentini M., Roussel M.F., Sherr C.J.,
 RA Look A.T.;
 RT "Genomic organization, chromosomal localization, and independent
 RT expression of human cyclin D genes.";
 RL Genomics 13:565-574(1992).
 CC -!- FUNCTION: Essential for the control of the cell cycle at the G1/S
 CC (start) transition.
 CC -!- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
 CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
 CC imparts substrate specificity to the complex.
 CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
 CC
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL; M90813; AA51926.1; -;
 DR EMBL; X68452; CAA48493.1; -;
 DR EMBL; D13639; BAA02802.1; -;
 DR EMBL; AF518005; AAM54041.1; -;
 DR EMBL; BC010958; AAH10958.1; -;
 DR EMBL; M88083; AA51928.1; -;
 DR EMBL; M88080; AA51928.1; JOINED.
 DR EMBL; M88081; AA51928.1; JOINED.
 DR EMBL; M88082; AA51928.1; JOINED.
 DR PIR; A42822; A42822.
 DR Genew; HGNC:1583; CCND2.
 DR GK; P30279; -;
 DR MIM; 123833; -;
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR004367; Cyclin_Cterm.
 DR InterPro; IPR006671; Cyclin_N.
 DR Pfam; PF0134; cyclin; 1.
 DR Pfam; PF02984; cyclin; 1.
 DR SMART; SM00385; CYCLIN; 1.
 DR PROSITE; PS00292; CYCLIN; 1.
 KW Cyclin; Cell cycle; Cell division; Multigene family.
 FT CONFLICT 166 167 KL -> NV (IN REF. 6).
 FT CONFLICT 224 224 T -> H (IN REF. 6).
 SQ SEQUENCE 289 AA; 33067 MW; E4ESFEF476D76D90 CRC64;
 Query Match 14.7%; Score 232; DB 1; Length 289;
 Best Local Similarity 28.0%; Pred. No. 3e-12;
 Matches 89; Conservative 50; Mismatches 111; Indels 68; Gaps 16;
 QY 8 LSLCTESN-----VDDEGMIVDETIETISIPQMGFSQSESEIIMEMVEKEKQHLPSDD 62
 DB 1 MELLCEVDPVRAVDRNLRD-----DVLQNLITIEERYLPQCS 42
 QY 63 YIKRLSGDLNNGRRDALNIWKA CEVHQFGLCFCLAMNYLDRLFLSHVLDLPQSGKI 122
 DB 43 YFKCVQK-DIQPYM-RRWATMWEVCEBQKCEEEVFLAMNYLDRLFLA--GVPTPKSH- 97
 QY 123 LQLLAVACLSLAAKIEETEVPMLIDQVGPDPVFEAKSVQRMELL-----VLNKLKWL 177
 DB 98 LQLLGAVCMFLASKLKETS-PL-----TAEKLCIYTDNSIKPQELLEWELVLGKLKWL 151
 QY 178 RAITPCSYIRYFLRKMSKDCQPSNTLSKLVQV-IASITTKGIDFLFEPSE-AAAAVAL 235
 DB 152 AAVTPHDFIEHLRLKPQ--QREKSLIRKHAQTFLCATDFKFMYPSPMIATGSGVA 209
 QY 236 SVSGELQRFVHFNSSPSPFLSLQK-----ERVKIKGEMIES-----DGS 275
 DB 210 AICGLQDDEEVSLTCDALTELLAKITNTDVCCLKACQEI EAVLLNSLQYRQDQDGS 269
 QY 276 ---DLCSQ--TPNGVLEV 288
 DB 270 KSEDELDAQASTPTDVRDI 287
 RESULT 13
 CG2D_CHICK STANDARD; PRT; 291 AA.
 AC P49706;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE GI/S-specific cyclin D2.
 GN CCND2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96144302; PubMed=8566807;
 RA Li H., Grenet J., Kidd V.J.;
 RL "Structure and gene expression of avian cyclin D2."
 RL Gene 167:341-342(1995).
 CC -!- FUNCTION: Essential for the control of the cell cycle at the G1/S
 CC (start) transition.
 CC -!- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
 CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
 CC imparts substrate specificity to the complex.
 CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
 CC
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 CC -----
 DR EMBL; U28980; AAA96955.1; -;
 DR PIR; JC4579; JC4579.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR004367; Cyclin Cterm.
 DR InterPro; IPR006671; Cyclin_N.
 DR Pfam; PF00134; cyclin; 1.
 DR Pfam; PF02984; cyclin C; 1.
 DR SMART; SM00385; CYCLIN; 1.
 DR PROSITE; PS00292; CYCLIN; 1.
 KW Cyclin; Cell cycle; Cell division; Multigene family.
 SQ SEQUENCE 291 AA; 33163 MW; 43A7E646AFAF3109 CRC64;

 Query Match 14.2%; Score 224.5; DB 1; Length 291;
 Best Local Similarity 30.1%; Pred. No. 1.3e-11;
 Matches 85; Conservative 46; Mismatches 104; Indels 47; Gaps 16;
 QY 8 LSLICTESNVDEGMIVDTPTTETPISIPQMGFSQSEEEIIMEMVEKEKHLPSDDYIKRL 67
 Db 1 MELLCE-----VD--PMRRALDPNLLY--DDRVLHLLTTEERYLPQCSYFKCV 47
 QY 68 RSGDLDLN-VGRDALNWIWKAQVHGFGLFCFLAMNYLDRLFLSVHDLPSGKWLQLL 126
 Db 48 QK---DIQPFMRWATWMLVCEEQCEEVEFPFLAMNYLDRLFLAV--VPTRK-CHLQLL 101
 QY 127 AVACLSLAAKIBETEVEFMILDIQVGPQVFFAKSVQRMELL-----VLNKLKWRIRAIT 181
 Db 102 GAVCMFLASKLKET-IPL-----TAEKLCIYTDNSIKPQELLEWELVVLGKLKNNLAAYT 155
 QY 182 PCSYIRYFLRKMSKCDQEPSNTLI---SRSLQVIASITTKGIDFLFRPSE-AAAVALSV 237
 Db 156 PHDFEHLIRKULP-----PKDKLILIRKHAQTIFALCATDFNFAMYPSPMIATGSGVRAI 211
 QY 238 SGELQVRHFDNS-SFSPFLSLQK-----ERVKKIGEMIES 272
 Db 212 CG-LQLDDGURSLGSDSLDFLAKITSTVDVCLKACQEQIES 252
 RESULT 14
 CGD2 XENLA
 ID CGD2 XENLA STANDARD; PRT; 291 AA.
 AC P53782;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE G1/S-specific cyclin D2.
 GN CCND2.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cockerill M.J., Hunt T.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97380591; PubMed=9237366;
 RA Taieb F., Jessus C.;
 RL "Xenopus cyclin D2: cloning and expression in oocytes and during
 RT early development."
 RL Biol. Cell 88:99-111(1996).
 CC -!- FUNCTION: Essential for the control of the cell cycle at the G1/S
 CC (start) transition.
 CC -!- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
 CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
 CC imparts substrate specificity to the complex.
 CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
 CC
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 CC -----
 DR EMBL; X89476; CAA61665.1; -;
 DR EMBL; X83503; CAA58493.1; -;
 DR PIR; S57925; S57925.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR004367; Cyclin Cterm.
 DR InterPro; IPR006671; Cyclin_N.
 DR Pfam; PF00134; cyclin; 1.
 DR Pfam; PF02984; cyclin C; 1.
 DR SMART; SM00385; CYCLIN; 1.
 DR PROSITE; PS00292; CYCLIN; 1.
 KW Cyclin; Cell cycle; Cell division; Multigene family.
 SQ SEQUENCE 291 AA; 32959 MW; 9A290F04F1531E89 CRC64;

 Query Match 13.9%; Score 220.5; DB 1; Length 291;
 Best Local Similarity 27.6%; Pred. No. 2.8e-11;
 Matches 79; Conservative 49; Mismatches 103; Indels 55; Gaps 13;
 QY 8 LSLICTESNV-----DDEGMIVDTPTTETPISIPQMGFSQSEEEIIMEMVEKEKHLPSDD 62
 Db 1 MELLCEGDTVRRAPQDPALLLD-----DRVLHLLTTEERYLPQCS 42
 QY 63 YIKRLRSGDLDLN-VGRDALNWIWKAQVHGFGLFCFLAMNYLDRLFLSVHDLPSGKWL 121
 Db 43 YFKCVQK---DIQPFMRWATWMLVCEEQCEEVEFPFLAMNYLDRLFLAV--VPTRK-C 96
 QY 122 ILQLLAVACLSLAAKIBETEVEFMILDIQVGPQVFFAKSVQRMELL-----VLNKLKWR 176
 Db 97 HLQLLGAVCMFLASKLKET-IPL-----TAEKLCIYTDNSIKPQELLEWELVVLGKLKNN 150
 QY 177 LRATPGSYIRYFLRKMSKCDQEPSNTLI---SRSLQVIASITTKGIDFLFRPSE-AAAA 232
 Db 151 LAAVTPEHDFEHLIRKULP-----PKDKLILIRKHAQTIFALCATDFNFAMYPSPMIATGS 206
 QY 233 VALSVSGELQVRHFDNS-SFSPFLSLQK-----ERVKKIGEMIES 272
 Db 207 VGAALCGLQLDVGTSLSGSDSLDFLAKITSTVDVCLKACQEQIES 252
 RESULT 15
 CGE1 HUMAN
 ID CGE1 HUMAN STANDARD; PRT; 410 AA.
 AC P24864; Q14091; Q8NFG1; Q92501;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE G1/S-specific cyclin E1.

GN CCNE1 OR CCNE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 8-410 FROM N.A.
RX MEDLINE=92005673; PubMed=1833068;
RA Koff A., Cross F., Fisher A., Schumacher J., le Guellec K.,
RA Philippe M., Roberts J.M.;
RT "Human cyclin E, a new cyclin that interacts with two members of the
RT CDC2 gene family,"
RL Cell 66:1217-1228(1991).
RN [2]
RP SEQUENCE OF 8-410 FROM N.A.
RX MEDLINE=92005671; PubMed=1833066;
RA Lew D.J., Dulic V., Reed S.I.;
RT "Isolation of three novel human cyclins by rescue of G1 cyclin (Cln)
RT function in yeast,"
RL Cell 66:1197-1206(1991).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM E1L).
RA Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Wittrak L.A., Nickerson D.A.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM E1L).
RX MEDLINE=22349257; PubMed=12477937;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences,"
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 1-42 FROM N.A.
RX MEDLINE=9626347; PubMed=8649818;
RA Geng Y., Eaton E.N., Picon M., Roberts J.M., Lundberg A.S.,
RA Gifford A., Sarter C., Weinberg R.A.;
RT "Regulation of cyclin E transcription by E2Fs and retinoblastoma
RT protein,"
RL Oncogene 12:1173-1180(1996).
RN [6]
RP SEQUENCE OF 281-370 FROM N.A.
RA Li H., Lahti J.M., Valentine M., Saito M., Reed S.I., Look T.,
RA Kidd V.J.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [7]
RP ALTERNATIVE SPLICING.
RX MEDLINE=94266993; PubMed=8207080;
RA Sewing A., Reenicke V., Buerger C., Funk M., Mueller R.;
RT "Alternative splicing of human cyclin E,"
RL J. Cell Sci. 107:581-588(1994).
RN [8]
RP PHOSPHORYLATION OF THR-395.
RX MEDLINE=97015119; PubMed=8861947;
RA Won K.A., Reed S.I.;

RT "Activation of cyclin E/CDK2 is coupled to site-specific
RT autophosphorylation and ubiquitin-dependent degradation of cyclin E,"
RL EMBO J. 15:4182-4193(1996).
RN [9]
RP TISSUE SPECIFICITY.
RX MEDLINE=99054678; PubMed=9840943;
RA Zariwala M., Liu J., Xiong Y.;
RT "Cyclin E2, a novel human G1 cyclin and activating partner of CDK2 and
RT CDK3, is induced by viral oncoproteins,"
RL Oncogene 17:2787-2798(1998).
CC -i- FUNCTION: Essential for the control of the cell cycle at the G1/S
CC (start) transition.
CC -i- SUBUNIT: Interacts with a member of the CDK2/CDK protein kinases
CC to form a serine/threonine kinase holoenzyme complex. The cyclin
CC subunit imparts substrate specificity to the complex. Interacts
CC with retinoblastoma binding protein 3 and retinoblastoma-like
CC protein 1.
CC -i- SUBCELLULAR LOCATION: Nuclear.
CC -i- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=E1L;
CC IsoId=P24864-1; Sequence=Displayed;
CC Name=E1S;
CC IsoId=P24864-2; Sequence=VSP_001253;
CC Note=Lacks 49 residues within the cyclin box and cannot complex
CC with CDK2;
CC -i- TISSUE SPECIFICITY: Highly expressed in testis and placenta. Low
CC levels in bronchial epithelial cells.
CC -i- PTM: PHOSPHORYLATION BY CDK2 TRIGGERS ITS RELEASE FROM CDK2 AND
CC DEGRADATION VIA THE UBIQUITIN PROTEASOME PATHWAY (BY SIMILARITY).
CC -i- SIMILARITY: Belongs to the cyclin family. Cyclin E subfamily.
CC -----
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CC -----
CC EMBL; M73812; -; NOT ANNOTATED CDS.
CC EMBL; M74093; -; NOT ANNOTATED CDS.
CC EMBL; AF518727; AA554043.1; ALT_INIT.
CC EMBL; BC035498; AA35498.1; -.
CC EMBL; X95406; CAA64687.1; -.
CC EMBL; X95406; CAA64688.1; -.
CC EMBL; U40788; AAA83269.1; -.
CC EMBL; U40787; AAA83269.1; JOINED.
CC PIR; A40270; A40270.
CC Genew; HGNC:1589; CCNE1.
CC GK; P24864; -.
CC MIM; 123837; -.
CC GO; GO:0005634; C:nucleus; NAS.
CC GO; GO:0000082; P:G1/S transition of mitotic cell cycle; NAS.
CC InterPro; IPR006670; Cyclin.
CC InterPro; IPR004367; Cyclin Cterm.
CC InterPro; IPR006671; Cyclin_N.
CC Pfam; PF00134; cyclin; 1.
CC Pfam; PF02984; cyclin_c; 1.
CC SMART; SM00385; CYCLIN; 1.
CC PROSITE; PS00292; CYCLINS; 1.
CC Cyclin; Cell cycle; Cell division; Alternative splicing;
CC Phosphorylation; Nuclear protein.
CC MOD_RES; 395 395
CC FT VARSPLIC 154 196
CC FT PHOSPHORYLATION.
CC FT Missing (in isoform E1S).
CC FT /FTid=VSP_001253.
CC FT L -> M (IN REF. 5).
CC FT CONFLICT 281 281
CC SEQUENCE 410 AA; 47077 MW; 424DF0B253B7047E CRC64;
Query Match 11.9%; Score 188.5; DB 1; Length 410;
Best Local Similarity 26.0%; Pred. No. 2.1e-08;
Matches 71; Conservative 49; Mismatches 102; Indels 51; Gaps 12;

Search completed: March 23, 2004, 16:38:03
Job time : 19 secs

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OM protein - protein search, using sw model

Run on: March 23, 2004, 16:34:50 ; Search time 46 Seconds
(without alignments)
2112.600 Million cell updates/sec

Title: US-09-530-209A-2
Perfect score: 1583
Sequence: 1 MAENLESLCTESNVDD.....SACFSFKYTHDSSSYTHLS 308

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mbc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1583	100.0	308	10 Q9XFR7	Q9xfr7 arabidopsis
2	1579	99.7	308	10 Q9FKP7	Q9fkp7 arabidopsis
3	1565	98.9	308	10 Q8LGA1	Q8lga1 arabidopsis
4	954	60.3	317	10 Q9LX96	Q9lxx6 arabidopsis
5	722.5	45.6	354	10 Q9ZRX9	Q9zrx9 nicotiana t
6	660.5	41.7	372	10 P93103	P93103 chenopodium
7	653.5	41.3	382	10 Q8L6U0	Q8l6u0 daucus caro
8	621.5	39.3	358	10 Q8S524	Q8s524 zea mays (m
9	614.5	38.8	356	10 Q8SBC0	Q8sbc0 oryza sativ
10	554.5	35.0	390	10 Q8S522	Q8s522 zea mays (m
11	521.5	32.9	356	10 Q8LH88	Q8lha8 oryza sativ
12	440.5	27.8	315	10 Q8GVE0	Q8gve0 helianthus
13	440	27.8	360	10 Q8GS62	Q8gs62 physcomitre
14	409	25.8	350	10 Q7XAB6	Q7xab6 euphorbia e
15	391	24.7	330	10 Q9SNV2	Q9snv2 antirrhinum
16	390.5	24.7	343	10 Q9SNV1	Q9snv1 antirrhinum

17	379	23.9	364	10 Q9SMD5	Q9smd5 lycopersico
18	379	23.9	373	10 Q9ZRX8	Q9zrx8 nicotiana t
19	378	23.9	352	10 Q8LK74	Q8lk74 lagenaria l
20	373.5	23.6	368	10 Q9SXN7	Q9sxn7 nicotiana t
21	370.5	23.4	367	10 Q9ZRX7	Q9zrx7 nicotiana t
22	370.5	23.4	380	10 Q8LK73	Q8lk73 lagenaria l
23	364.5	23.0	198	10 Q8S521	Q8s521 zea mays (m
24	363	22.9	376	10 Q8GZU3	Q8gzu3 populus tre
25	362.5	22.9	367	10 Q9FGQ7	Q9fgq7 arabidopsis
26	359.5	22.7	355	10 Q7XAB7	Q7xab7 euphorbia e
27	359.5	22.7	384	10 Q82136	Q82136 pisum sativ
28	357.5	22.6	357	10 Q8GVD9	Q8gvd9 helianthus
29	357.5	22.6	378	10 Q9XG63	Q9xg63 medicago sa
30	354.5	22.4	386	10 Q40338	Q40338 medicago sa
31	353	22.3	361	10 Q9SN11	Q9sn11 arabidopsis
32	352.5	22.3	359	10 Q9S7H9	Q9s7h9 lycopersico
33	351.5	22.2	361	10 Q9SNV0	Q9snv0 antirrhinum
34	346.5	21.9	336	10 Q9SMD4	Q9smd4 lycopersico
35	345.5	21.8	371	10 Q84V88	Q84v88 populus alb
36	344	21.7	289	10 Q8GUV7	Q8guv7 populus alb
37	343.5	21.7	308	10 Q8LFW3	Q8lpw3 helianthus
38	323.5	20.4	222	10 Q9XG64	Q9xg64 medicago sa
39	305	19.3	302	10 Q9ZRX04	Q9zrx04 arabidopsis
40	302	19.1	349	10 Q82678	Q82678 chenopodium
41	291.5	18.4	349	10 Q8S523	Q8s523 zea mays (m
42	285.5	18.0	322	10 Q8H339	Q8h339 oryza sativ
43	285.5	16.8	321	10 Q9SZF6	Q9szf6 arabidopsis
44	260.5	16.5	291	13 Q8AVQ4	Q8avq4 xenopus lae
45	255	16.1	291	13 Q8QFP4	Q8qfp4 brachydanio

ALIGNMENTS

RESULT 1

Q9XFR7 ID Q9XFR7 PRELIMINARY; PRT; 308 AA.
AC Q9XFR7;
DT 01-NOV-1999 (TREMREL. 12, Created)
DT 01-NOV-1999 (TREMREL. 12, Last sequence update)
DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
DE D-type cyclin.
GN CYC04.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA de Veylder L., De Almeida Engler J., Burssens S., Manevski A.,
RA Lescure B., Van Montagu M., Engler G., Inze D.;
RT "A new D-type cyclin of Arabidopsis thaliana expressed during lateral
root primordia formation."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AJ131636; CAB41347.1;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR SMART; SM00385; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 308 AA; 34887 MW; 591ADA3361DDD63D CRC64;

Query Match 100.0%; Score 1583; DB 10; Length 308;
Best Local Similarity 100.0%; Pred. No. 1.3e-139;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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QY 121 WILLOLAVACLSAAKIEETVPMILDLQVGPQVFEAKSVORMELLVINKLWRLRAI 180
DB 121 WILLOLAVACLSAAKIEETVPMILDLQVGPQVFEAKSVORMELLVINKLWRLRAI 180
QY 181 TPCSYIRYFLRMKSKCDQEPNTLISRSLOVIASTTKGIDLEFRPSEAAAAVALSVSGE 240
DB 181 TPCSYIRYFLRMKSKCDQEPNTLISRSLOVIASTTKGIDLEFRPSEAAAAVALSVSGE 240
QY 241 LORVHFONSSPFLSLLOKERVKKIGEMIESDGLCSQTPNGVLEVSACCFKTHDS 300
DB 241 LORVHFONSSPFLSLLOKERVKKIGEMIESDGLCSQTPNGVLEVSACCFKTHDS 300
QY 301 SSSYTHLS 308
DB 301 SSSYTHLS 308

RESULT 4
Q9LX96 PRELIMINARY; PRT; 317 AA.
AC Q9LX96;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cyclin protein-like.
GN F12B17.210.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bavan M., Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AL353995; CAB89399.1; -.
DR PIR; T49995; T49995.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
DR Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 317 AA; 35910 MW; 07616F848092711 CRC64;

Query Match 60.3%; Score 954; DB 10; Length 317;
Best Local Similarity 64.8%; Pred. No. 9, 1e-81;
Matches 212; Conservative 23; Mismatches 58; Indels 34; Gaps 8;

QY 4 ENLESLCTESNVDDGMIVDTPETIEISIPQMGFSQSEEEIMEMVEKEKQHLPSDDY 63
DB 3 EFMEPNLV---SNFDEKSNVDTR---SIFQMGF-PLESEIVREMIERQHSPRDY 55
QY 64 IKRLRSGLDLNVRDALNWIKACEVHQFGLPCFLAMNYLDRLSVHDLPSGKGWIL 123
DB 56 LKRLRGDLDLVN-RIQALGIWIKACEELQFGLCFLAMNYLDRLSVHDLPSGKATV 114
QY 124 QLAVACLSAAKIEETVPMILDLQVGPQVFEAKSVORMELLVINKLWRLRAITPC 183
DB 115 QLAVACLSAAKIEETVPMILDLQVGPQVFEAKSVORMELLVINKLWRLRAITPC 174
QY 184 SYIRYFLRMKSKCDQEPNTLISRSLOVIASTTK-----GIDFLEF 224
DB 184 SYIRYFLRMKSKCDQEPNTLISRSLOVIASTTK-----GIDFLEF 224

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DB 175 SYRYFISKINGYDQEPHSLVTRSLQVIASTTKGDRGLGLFFPKGVLIIVDWAGIDFLEF 234
QY 225 RPSEAAAAVALSVSGELQRVHFDNSSFPLSLLOKERVKKIGEMIESDGLCSQTPNG 284
DB 235 RASEIAAAVALSVSGE---HFDFKFSFSSFSLEKERVKKIGEMIERDGGSSSSSTPN 290
QY 285 -VLEVSACCF--SPKTHDSSSSYTHLS 308
DB 291 TVLQFKRRYSHSLSTASVSSSLTSL 317

RESULT 5
Q9ZRX9 PRELIMINARY; PRT; 354 AA.
AC Q9ZRX9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cyclin D2.1 protein.
GN CYCD2.1.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99097070; PubMed=9880377;
RA Sorrell D.A., Combettes B., Chaubert-Gigot N., Gigot C., Murray J.A.H.;
RT "Distinct Cyclin D Genes Show Mitotic Accumulation or Constant Levels
RT of Transcripts in Tobacco Bright Yellow-2 Cells.";
RL Plant Physiol. 119:343-351 (1999).
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AJ011892; CAA09852.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
DR Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 354 AA; 39714 MW; 18363A0E786E89BF CRC64;

Query Match 45.6%; Score 722.5; DB 10; Length 354;
Best Local Similarity 48.1%; Pred. No. 4, 7e-59;
Matches 164; Conservative 60; Mismatches 76; Indels 41; Gaps 10;

QY 1 MAEENL-----ELSLCTESNV-----DDEGMIVDTPETIEISIPQMGFSQ-----S 41
DB 1 MAADNIYDFVASNLLCTETKSLCFDDVDSLTTISQQNIETKSDLSFNNGIRSEPLIDLFS 60
QY 42 ESEETIMEMVEKEKQHLPSDDYIKRLRSGLDLNVRDALNWIKACEVHQFGLPCFL 101
DB 61 LSEECLSFVQREMEFLPKDDYVERLSRGLDLSV-RKEALDWILKAHMHYGFGLSFCL 119
QY 102 ANNYLDRLSVHDLPSGKGWILQLAVACLSAAKIEETVPMILDLQVGDQFVFEAKS 161
DB 120 SINYLDRLSVHDLPSRKTWTVQLLAVACLSAAKMEETINVELTVDLQVGDQFVFEK 179
QY 162 VORMELLVINKLWRLRAITPCSYIRYFLRMKSKCDQEPNTLISRSLOVIASTTKGIDF 221
DB 180 IQRMELLVSLTKWRQAYTPFTFYPMRWKNG-DQIPSRPLISGWLILSIIRSIDF 238
QY 222 LFRFSEAAAAVALSVSGELQRVHFDNSSFPLSL-LQKERVKKIGEMIE----- 271
DB 239 LFRFSESEAAASVAMSVSGEIQAKIDKA--MPCFFIHLDKGRVQKVELIQDLTATITT 296
QY 272 SDGSLCSQTPNGVLEVSACCFKTHD-----SSSYT 305
DB 272 SDGSLCSQTPNGVLEVSACCFKTHD-----SSSYT 305

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RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC	-I- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR	EMBL; AB080248; BAB85522.1; --
DR	Graneine; Q85BC0; --
DR	GO; GO:0005634; C:nucleus; IEA.
DR	GO; GO:0000910; P:cytokinesis; IEA.
DR	GO; GO:0000074; P:regulation of cell cycle; IEA.
DR	InterPro; IPR006670; Cyclin.
DR	InterPro; IPR004367; Cyclin_Cterm.
DR	Pfam; PF001134; cyclin; 1.
DR	Pfam; PF02984; cyclin; C; 1.
DR	SMART; SM00385; CYCLIN; 1.
DR	PROSITE; PS00292; CYCLINS; 1.
KW	Cell cycle; Cell division; Cyclin.
SQ	SEQUENCE 356 AA; 38937 MW; 502AF4EB9CE8BCEA CRC64;
Query Match 38.8%; Score 614.5; DB 10; Length	
Best Local Similarity 45.3%; Pred. No. 6e-49;	
Matches 134; Conservative 51; Mismatches 72; Indels	
Qy	24 VDPTPIRISIPQMGSQSEEEIIMVVEKEKQHLPSDDYIKRLRS----
Db	54 VDVGVDFAVP-----SEECVARLIVETADHWPRDYAERLRAG
Qy	80 DALNWIWKACEVHQFGFLCFCLAMNYLDRLFVSHDLFSGKWIQLQLALA
Db	105 DAIDWIWKVHSYYSFAPLTACLAENVYLDRLFSLYQLPGDKMMTQLLA
Qy	140 TEVPMILDLQVGDPQPFVFAKSVQRMELLVNLKWLKRLRAITPCSYH
Db	165 TDVPQSLDLQVGERYVFEAKTIQRMELLVLSTLKWRMQAVTPFSYV
Qy	200 PSNTLISRSQVIASTTKGIDIEFESEAAAAVALSVSGELQVHF
Db	224 PSGRSALLSELILCTARGTECLGFRSETAATAVAAVVGEEHAA---
Qy	260 KERVKKIGEMIESDG-----SDLCSQTPTNGVLEVSACFCF
Db	274 KERMSHCQEVIAQAMELIHPKSPSVFVSSIPRPTGVLD--AAGCL
RESULT 10	
Q88522	Q88522 PRELIMINARY; PRT; 390 AA.
ID	Q88522;
AC	Q88522;
DT	01-JUN-2002 (T-EMBLrel. 21, Created)
DT	01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT	01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE	D-type cyclin.
GN	CYC4.
OS	Zea mays (Maize).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae
OC	PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX	NCBI_TaxId=4577;
RP	[1]
RN	SEQUENCE FROM N.A.
RA	STRAIN=cv. Hi-II;
RC	Tao Y., Lowe K., Gregory C., Coughlan S.J., Gordon-Kamm W
RT	"Isolation of a family of D-type cyclins from maize that
RT	conserved and unique characteristics.";
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC	-I- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR	EMBL; AF351191; AAL83928.1;
DR	GO; GO:0005634; C:nucleus; IEA.
DR	GO; GO:0000910; P:cytokinesis; IEA.
DR	GO; GO:0000074; P:regulation of cell cycle; IEA.
DR	InterPro; IPR006670; Cyclin.
DR	InterPro; IPR004367; Cyclin_Cterm.
DR	Pfam; PF001134; cyclin; 1.
DR	Pfam; PF02984; cyclin; C; 1.

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DR SMART, SM00395; CYCLIN; 1.
KW PROSITE; PS00292; CYCLINS; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 390 AA; 42016 MW; 1CE006BE20DAF70 CRC64;

Query Match      35.0%; Score 554.5; DB 10; Length 390;
Best Local Similarity 39.1%; Pred. No. 2.8e-43;
Matches 135; Conservative 52; Mismatches 89; Indels 69; Gaps 29;

QY 10 LLCTESNVD-----DEGMIVDTPTPEISIPQMGFSQS-----ESEEIMEMVEK 53
DB 13 LLCAEHSLSLWYDE---EEEELEAVGRRGRSPGYGDDFGADLFPQSEECVAGLVER 68
QY 54 EKQHPDSDDIKRLSGDLDLNVGRRDALNWIWKAACEVHQFGPLCFCLAMNYDLRFLSVH 113
DB 69 ERDHMPGPCYDRLRGGGGCLCV-RREAVDWIKAYTHHFRPLTAYLAVNYDLRFLSL 127
QY 114 DLPSGKMWILLQILAVACLSAAKTEETEVPMILDIQVGDPOFVFEAKSVQRMELLIVLNL 173
DB 128 EVPDGKOWMTQLLAVACVSLAAKMEETAVPOCLDQVGDARVFEAKTVQRMELLIVLT 187
QY 174 KWLRLAITPCSYIRYIRKMSK-CDQEPSNTLISRLQVIASLTGKIDFLFRPSEAAA 232
DB 188 NWRMHAVTPFSYDYFLNKLNGSGSTAPRSCWLLQSAELILRAARGTCVGFRRPSEIAA 247
QY 233 VALSVSGELQR-----VHFNSFSPLFSLLOKERVKKIGEMTESDGSDLCL----- 278
DB 248 VAAAVGVDVDDAGVENACCAHVD-----KERVURCQEAIGMASSAAIDGDA 295
QY 279 -----SQTPNGVLVSACCFSPFKTHDSSS 303
DB 296 TVPPKSARRRSPVPVPVQSPGVGLD-AAACLSYRSEAAATA 339

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RESULT 11
ID Q8LHA8
ID Q8LHA8 PRELIMINARY; PRT; 356 AA.
AC Q8LHA8;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE P0594D10.18 protein.
DE P0594D10.18.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_taxid=39947;
RX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC
RT clone:P0594D10.18";
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
RC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AP004380; BAC10182.1; -.
DR Gramene; Q8LHA8; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
DR Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 356 AA; 39176 MW; 8E8A8B8DA7A39EEE CRC64;

Query Match 32.9%; Score 521.5; DB 10; Length 356;
Best local Similarity 44.4%; Pred. No. 3e-40;

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	Matches	119,	Conservative	49,	Mismatches	89,	Indels	11,	Gaps	6,
QY	42	ESEIIIMVYEKEQHLPDSDYIKRLSRSGDLNLNVGRDALNIWKAACEVHQFGPLCFCL	101	:	:	:	:	:	:	:
Db	60	DSDEFVALLVEKEMDHPQRGYLEKELEGLGLECS-WRKDAIDMICKVHSYVNFGLSLYL	118	:	:	:	:	:	:	:
QY	102	AMNYLDREFLSVDLPSCKGWLLOLLAVACLSLAAKTEETVPMLIDLGVGDPOFVPEAKS	161	:	:	:	:	:	:	:
Db	119	AVNYLDRFLSSFNLPDHESMMOQLSVCSLSLATKMEETVVPMDLVQVDAEYVFARH	178	:	:	:	:	:	:	:
QY	162	VORMELLVLNKLKWRLEAITPCSYIRYFLFKMKSCDOEPSNTILSRSLQVIASITTKGIDF	221	:	:	:	:	:	:	:
Db	179	IKRMELIVMKTALKRWLQAQVTPFSFIQVFLDKENE-GKPSPYTLASWCSDLTVGTLKDSRF	237	:	:	:	:	:	:	:
QY	222	LFRPFEAAAVALSVSGELORVHDNPFSSPFLSKLOKRVKKIGB-MTES-----DG	274	:	:	:	:	:	:	:
Db	238	LSRFPGEIAAVALVAENQFLVF-NSALGEGSEIPVNKEGMVMRCVELMVKEKALVKKIRN	296	:	:	:	:	:	:	:
QY	275	SDFCSTPTNGVLEV-SACCFSPFKTHDSS	301	:	:	:	:	:	:	:
Db	297	NNASSSVPHSPITVLDAACTFSRSDTTT	324	:	:	:	:	:	:	:

RESULT 12

Q8GVEO PRELIMINARY; PRT; 315 AA.

ID	Q8GVEO	
AC	Q8GVEO;	
DT	01-MAR-2003 (TrEMBLrel. 23, Created)	
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	Cyclin D1.	
DE	CYC1D.1.	
GN	Helianthus tuberosus (Jerusalem artichoke).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;	
OC	cambiumlids; Asterales; Asteraceae; Asteroideae; Heliantheae;	
OC	Helianthus.	
OX	NCBI_TaxId=4233;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Freeman D., Murray J.A.H.;	
RT	"Isolation, characterization and expression of cyclin and cyclin-	
RT	dependent kinase genes in Jerusalem Artichoke (Helianthus	
RT	tuberosus)".	
NL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AY063460; AAI47479.1; -	
DR	GO; GO:0005634; C:nucleus; IEA.	
DR	GO; GO:0000074; P:regulation of cell cycle; IEA.	
DR	InterPro; IPR006670; Cyclin.	
DR	InterPro; IPR004367; Cyclin term.	
DR	InterPro; IPR006671; Cyclin_N.	
DR	Pfam; PF00134; cyclin; i.	
DR	Pfam; PF02984; cyclin_C; i.	
DR	SMART; SM00385; CYCLIN; i.	
DR	PROSITE; PS00292; CYCLINS; i.	
SQ	SEQUENCE 315 AA; 35651 MW; 8F35A49F1097C308 CRC64;	

	Query Match	27.8%	Score 440.5	DB 10	Length 315
	Best Local Similarity	36.6%	Pred. No. 9.6e-33		
	Matches 111	Conservative 59	Mismatches 102	Indels 31	Gaps 9
Qy	10	LLCTESNVDDGMLVDETETIEISIPQWGSQS--ESEETIMEMVETKEQHLPSDDYIKLR	68		
Db	12	LLCCE---DSGLSGDDRPEC---YDEFSGDGDDSTAEFTQEQRKVPFGDIYVERFQ	64		
Qy	69	SGDLNLNVRDRDALNIWKACEVHQFGPLCFCLAMNYLDRFLSVHDLPSCKGWLQLLAV	128		
Db	65	SQVLDAS--AREESVAMLLKQRYGVGQPLTAYLSVNYLDRFFYICRGFPVANGWPLQLLSV	123		
Qy	129	ACLSLAAKTETETVPMILDLQVGDPQVFPEAKSVQRMELLVNKLKWRDAITPCSVIRY	188		
Db	124	ACLSLAAKMBETLIPSIDLQVGKAYITPEKTIIRMEFLVSLVDWRLSVTFPFGIFG	183		

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QY 189 FLKMSKCDQEPSNT-----LISRSLOVIATTKGIDFLFRPSEAAVAVALSVGELQRV 244
DQ 184 FSHKI-----DPSGMYTGFLISRATQIILNIQASLELWPSICAAATILCAASDLKSF 238
QY 245 HFNSFSPLF-SLLQKRVKIGEMIESDGLCSQTPNGV---LEVSACCFKTHDS 300
DQ 239 SLINADHAESWCGLSKEKTKCYRLV-----QSPKILPVHVRVMTARVSTESGDS 289
QY 301 SSS 303
DQ 290 SSS 292

RESULT 13
Q8GS62
ID Q8GS62 PRELIMINARY; PRT; 360 AA.
AC Q8GS62
DT 01-MAR-2003 (TREMREL. 23, Created)
DT 01-MAR-2003 (TREMREL. 23, Last sequence update)
DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
DE Cyclin D.
GN CYCD.
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Protonema;
RA Lorenz S., Reski R., Decker E.L.;
RT "Cell cycle genes in Physcomitrella patens.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Lorenz S., Reski R., Decker E.L.;
RT "Cell cycle genes in Physcomitrella patens.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ428953; CAD21955.1; -
DR EMBL; AJ488282; CAD32542.1; -
DR GO; GO:0005634; C.nucleus; IEA.
DR GO; GO:000074; P.regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin C; 1.
DR SMART; SM00385; CYCLIN; 1.
SQ SEQUENCE 360 AA; 40502 MW; 717BEA801824F067 CRC64;

Query Match 27.8%; Score 440; DB 10; Length 360;
Best Local Similarity 35.1%; Pred. No. 1.3e-32;
Matches 115; Conservative 57; Mismatches 118; Indels 38; Gaps 9;

QY 9 SLLCTESVDDDEGMIVDETPISIPQMGFSQS-----ESETIMMVEKQHLPS 60
DQ 10 SLYCAE---DVSGTAWNEEMCCADRVFSPAVFMDFVEDDEAIAITLKLKEAQFME 66
QY 61 DDIYKRLSGDLDLVNVRDALNWKACEVHQFGPLCFCLANVYLDRLSVHDLPSHGK 120
DQ 67 ADYLERYSQKLSLE-ARLAALEWLKLVHSFYNGSLTVALAVNYMDRLSYTFPEGKE 125
QY 121 WILQIIVACLSIAAKIETEVPMILDLQVGPQFVFEAKSVORMELLVNLKWLRLAI 180
DQ 126 WMLQLLSVACISIAAKWESDVPILLDFVQEEHIFEAHTIQRMELLVISTLEWRMGV 185
QY 181 TPCSYIRYFLRMKCDQSPSNTLSRSQVIASTTKGIDFLFRPSEAAVAVALSVSGE 240
DQ 186 TPFYSYVDFPHKLGVSDEL-LRLALLSRVSEIILKSIRVTTSLQYLPVVAAASIICALEE 244
QY 241 LQRVHFDN--SFSPLFSLLOKRVKIG-EMIESDGLC-----SQTPN 283
DQ 245 VTTITGDLRTFNEL--LVNVESVKDCYIDMRQSEIGPYCVRMGLKRLKHASEPQSPV 302

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QY 284 GVLEV-----SACCFKTHDSSSYT 305
DQ 303 GVLEAADVSPSGTGLGFSRSPDPVT 330

RESULT 14
Q7XAB6
ID Q7XAB6 PRELIMINARY; PRT; 350 AA.
AC Q7XAB6
DT 01-OCT-2003 (TREMREL. 25, Created)
DT 01-OCT-2003 (TREMREL. 25, Last sequence update)
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE Cyclin D3-1.
GN CYCD3-1.
OS Euphorbia esula (leafy spurge).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Malpighiales; Euphorbiaceae; Euphorbiaceae; Euphorbiae;
OC Euphorbia.
OX NCBI_TaxID=3993;
RN [1]
RP SEQUENCE FROM N.A.
RA Horvath D.P.;
RT "Cloning of cyclin D3 genes from Euphorbia esula.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY340589; AAQ19973.1; -
KW Cyclin.
SQ SEQUENCE 350 AA; 39835 MW; CF080P5E07C6C485 CRC64;

Query Match 25.8%; Score 409; DB 10; Length 350;
Best Local Similarity 34.1%; Pred. No. 9.7e-30;
Matches 115; Conservative 59; Mismatches 91; Indels 72; Gaps 13;

QY 9 SLLCTESVDDDEGMIVDETPISIPQMGFSQSSEEEIIMEM 50
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QY 51 VEKEQHLPSSDYIKRLSGDLDLN---VGRDALNWTWKACEVHQFGPLCFCLANVYL 106
DQ 63 SKQEQNL-----YKK-----LEINPLAKSRDADVNMKNVNAHVSFTALTSVLAVNFL 112
QY 107 DRFLSVHDLPSGKWLQIOLAVACLIAAKIETEVPMILDLQVGPQFVFEAKSVORME 166
DQ 113 DRFLSFDLQTEKPMWTLTAVACLSIAAKVETQVPLLDLQVDSKYVFEAKTIQME 172
QY 167 LLVNLKWLRLAITPCSYIRYFLRMKSKDCQ---EPSNTLSRSQVIASTTKGIDFL 223
DQ 173 LLVLTSLQWRNMPVPLSFIDYMTRELGLKDYLCWE---FIRCELIVLSIDMRFP 228
QY 224 FPPSEAAAVALSVSGELQRVHFDNSFSPLSL--OKERVKKTGEMI-----270
DQ 229 YLPFSIAAAILMHVINGIEPSLGDFFE-TQLFGILGIDKEKVNCRMIIELGSRVYGNQ 287
QY 271 ---ESDGLCSQTPNGVLEVSACCFKTHDSSSY 304
DQ 288 SNKRYKGS--PGSPNCVMDV-----SPSSDNSDSW 317

RESULT 15
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ID Q9SNV2 PRELIMINARY; PRT; 330 AA.
AC Q9SNV2
DT 01-MAY-2000 (TREMREL. 13, Created)
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
DE Cyclin D1.
GN CYCD1.
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Plantaginaceae; Antirrhineae; Antirrhinum.
OX NCBI_TaxID=4151;
RN [1]

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Search completed: March 23, 2004, 16:39:03
Job time : 49 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 23, 2004, 16:39:47 ; Search time 61 Seconds
(without alignments)
1426.633 Million cell updates/sec

Title: US-09-530-209A-2
Perfect score: 308
Sequence: 1 MAEENLELLCTESNVDE.....SACCFKTHDSSSYTHLS 308

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_23Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	228	74.0	308	3 AAG47103	Aag47103 Arabidops
2	207	67.2	287	3 AAG47104	Aag47104 Arabidops
3	207	67.2	308	2 AAY14071	Aay14071 Mitogenic
4	193	62.7	273	3 AAG47105	Aag47105 Arabidops
5	171	55.5	308	3 AAG23337	Aag23337 Arabidops
6	150	48.7	287	3 AAG23338	Aag23338 Arabidops
7	136	44.2	273	3 AAG23339	Aag23339 Arabidops
8	13	4.2	320	3 AAG23790	Aag23790 Arabidops
9	13	4.2	328	3 AAG23789	Aag23789 Arabidops
10	13	4.2	339	3 AAG23788	Aag23788 Arabidops
11	11	3.6	36	6 ABR98363	AbR98363 Tumour ce
12	11	3.6	36	7 ADC84709	Adc84709 MCF-7 bre
13	11	3.6	244	6 ABU70573	Abu70573 Human adi
14	11	3.6	295	2 AAR27114	Aar27114 pradi. 3/
15	11	3.6	295	2 AAR29310	Aar29310 Cyclin D1
16	11	3.6	295	2 AAR44802	Aar44802 Human cyc
17	11	3.6	295	2 AAR54044	Aar54044 bcl-1 pro
18	11	3.6	295	4 AAB90768	Aab90768 Human she
19	11	3.6	295	7 ADE55900	Ade55900 Rat Prote
20	11	3.6	295	7 ADE64090	Ade64090 Rat Prote
21	11	3.6	295	7 ADE55902	Ade55902 Human Pro
22	11	3.6	295	7 ADE55888	Ade55888 Rat Prote
23	11	3.6	295	7 ADE55896	Ade55896 Rat Prote
24	11	3.6	295	7 ADE55898	Ade55898 Human Pro
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30	11	3.6	295	7 ADE64091	Ade64091 Human Pro
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32	11	3.6	358	3 AAY79321	Aay79321 Maize cyc
33	11	3.6	358	7 ABR61588	AbR61588 Z. mays c
34	11	3.6	385	5 ABP41466	Abp41466 Human ova
35	11	3.6	618	2 AAW18571	Aaw18571 Human cyc
36	11	3.6	618	2 AAW74572	Aaw74572 Human cyc
37	11	3.6	647	2 AAW00926	Aaw00926 Human cyc
38	11	3.6	647	2 AAW74575	Aaw74575 Human cyc
39	11	3.6	660	2 AAW18570	Aaw18570 Human cyc
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ALIGNMENTS

RESULT 1
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AC AAG47103;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59333.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Tue Mar 23 17:02:01 2004

us-09-530-209a-2.Olig.rag

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PR	24-MAY-1999;	99US-0135623P.	PR	02-AUG-1999;	99US-0146389P.
PR	25-MAY-1999;	99US-0136021P.	PR	03-AUG-1999;	99US-0147038P.
PR	25-MAY-1999;	99US-0136392P.	PR	04-AUG-1999;	99US-0147204P.
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Query Match 67.2%; Score 207; DB 3; Length 287;
Best Local Similarity 100.0%; Pred. No. 7.4e-188;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 VPMLIDLQVGDQFVFPEAKSVQRMELLVNLKWLKRLAITPCSYIRYFLRKMSKCDQEPS 180
QY 202 NTLISRSLOVIASITTKGIDFLFRPSE 228
Db 181 NTLISRSLOVIASITTKGIDFLFRPSE 207

RESULT 3
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ID AAV14071 standard; protein; 308 AA.
XX
XX AAV14071;
XX
DT 16-JUL-1999 (first entry)
XX
DE Mitogenic cyclin CYCD4 protein sequence.
XX
KW Mitogenic cyclin; CYCD4; modulator; plant cell cycle; growth inhibitor;
KW plant cell division; cell growth; regulator; cell proliferation;
KW growth regulator; herbicide; cell division progression.
XX
OS Arabidopsis thaliana.
XX
FN WO9922002-A1.
XX
PD 06-MAY-1999.
XX
PF 23-OCT-1998; 98WO-EP006749.
XX
PR 24-OCT-1997; 97EP-00203303.
XX
(CROP-) CROPDESIGN NV.
XX
PI Inze D, De Veylder L, De Almeida J;
XX
DR WPI; 1999-312966/26.
XX
N-PSDB; AAX36897.
XX
DNA sequence encoding a mitogenic cyclin.
XX
Claim 1; Page 47-49; 57pp; English.
XX
This sequence is the mitogenic cyclin, CYCD4, of the invention. The DNA
sequence, vectors containing it, protein encoded by it, or antibodies
recognising the protein can be used for modulating plant cell cycle,
CC
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PR 20-JUL-1999; 99US-0144352P.
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XX KW hybridisation assay; genetic mapping; gene expression control; promoter;

XX KW termination sequence.

XX OS Arabidopsis thaliana.

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XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

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PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.

PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161932P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 4.2%; Score 13; DB 3; Length 339;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QLLAVACLSLAAK 136
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Db 128 QLLAVACLSLAAK 140

RESULT 11
ABR98363
ID ABR98363 standard; peptide; 36 AA.
XX
AC ABR98363;
XX
DT 17-SEP-2003 (first entry)
XX
DE Tumour cell growth inhibitor genetic suppressor element peptide SEQ:241.
KW Human; tumour cell growth inhibiting genetic suppressor element;
KW breast cancer; tumour; cytostatic; tumour cell growth inhibitor.
XX
OS Homo sapiens.
XX
PN WO2003008578-A2.
XX
PD 30-JAN-2003.
XX
PF 28-FEB-2002; 2002MO-US006254.
XX
PR 20-JUL-2001; 2001US-0306730P.
XX
PA (UNII ) UNIV ILLINOIS FOUND.
XX
PI Primiano T, Chang B, Roninson IB;
XX
WPI; 2003-248013/24.
XX
PT Identifying compounds that inhibit mammalian genes necessary for tumor
cell growth, useful for inhibiting tumor cell growth, by assaying for
expression or activity of several genes necessary for tumor cell growth.
XX
PS Claim 22; Page 67; 145pp; English.
XX
CC The present invention describes a method (M) for identifying a compound
(C) that inhibits growth of a mammalian cell. (M) involves culturing a
cell in the presence or absence of (C), assaying the cell for expression
or activity of one or more enriched genes (see Table 3 in the
specification, G1) that have not been previously implicated in cell
proliferation, and identifying (C) when expression or activity of at
least one of (G1) is lower in presence of (C) than in absence of (C).
CC Also described in a compound (I) that inhibits tumour cell growth and
mammalian cell expression or activity of (G1), identified by (M), where
(I) is not an inhibitor or RNA synthesis or protein synthesis. (C) and
(C) (I) have cytostatic activity and can be used as tumour cell growth
```

CC inhibitors. (M) is useful for identifying a compound that inhibits growth
 CC of a mammalian cell preferably a human tumor cell. (I) is useful for
 CC inhibiting tumor cell growth by inhibiting expression of (G1). (I) is
 CC useful for treating a disease or condition relating to abnormal cell
 CC proliferation or tumor cell growth. ACF18960 to ACF19187 and ABR98351 to
 CC ABR98436 represent sequences used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 36 AA;

Query Match 3.6%; Score 11; DB 6; Length 36;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 LAMNYLDRFLS 111
 |||||
 Db 25 LAMNYLDRFLS 35

RESULT 12

ADC84709
 ID ADC84709 standard; peptide; 36 AA.
 AC ADC84709;
 XX
 DT 01-JAN-2004 (first entry)
 DE MCF-7 breast cancer cell tumor library GSE peptide #13.
 XX
 KW cytostatic; cell proliferation; tumor; breast cancer cell;
 KW genetic suppressor element.
 XX
 OS Homo sapiens.
 XX
 PN WO2003007884-A2.
 XX
 PD 30-JAN-2003.
 XX
 PF 19-JUL-2002; 2002WO-US022868.
 XX
 PR 20-JUL-2001; 2001US-0306730P.
 PR 28-FEB-2002; 2002WO-US006254.
 XX
 PA (UNII) UNIV ILLINOIS FOUND.
 XX
 PI Primiano T, Chang B, Roninson IB;
 XX
 WPI; 2003-312622/30.
 N-PSDB; ADC84837.

Identifying compounds that inhibit mammalian genes necessary for tumor
 cell growth, useful for inhibiting tumor cell growth, comprises assaying
 for expression or activity of several genes necessary for tumor cell
 growth.

Claim 22; SEQ ID NO 241; 145pp; English.

The invention relates to a method of identifying a compound that inhibits
 growth of a mammalian cell, comprising culturing a cell in presence or
 absence of the compound, assaying the cell for expression or activity of
 one or several enriched genes that have not been previously implicated in
 cell proliferation, as given in specification, and identifying the
 compound when expression or activity of at least one of the enriched
 genes is lower in presence of the compound than in its absence. The
 method is useful for identifying a compound that inhibits growth of a
 mammalian cell preferably a human tumor cell. The compound is useful for
 inhibiting tumor cell growth by inhibiting expression of the genes. The
 compound is useful for treating a disease or condition relating to
 abnormal cell proliferation or tumor cell growth. This sequence
 represents a genetic suppressor element (GSE) peptide isolated from the
 MCF-7 breast cancer cell tumor library using the method of the invention.

Sequence 36 AA;

Query Match 3.6%; Score 11; DB 7; Length 36;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 LAMNYLDRFLS 111
 |||||
 Db 25 LAMNYLDRFLS 35

RESULT 13

ABU70573
 ID ABU70573 standard; protein; 244 AA.

AC ABU70573;

DT 10-JUN-2003 (first entry)

XX Human adipocyte Selected Interacting domain, SID, #204.

XX Human; prey; adipocyte; SID; selected interacting domain; anorectic;
 KW anti-diabetic; protein-protein interaction; diabetes;
 KW yeast 2-hybrid assay; metabolic disorder; obesity.
 XX

OS Homo sapiens.

PN WO200286122-A2.

PD 31-OCT-2002.

PF 14-MAR-2002; 2002WO-EP003768.

PR 14-MAR-2001; 2001US-0275734P.

XX (HYBR-) HYBRIGENICS.

XX Legrain P, Daviet L;

PI WPI; 2003-103412/09.

DR N-PSDB; ACA57117.

XX New complex between two interacting proteins in adipocyte cells, useful
 PT for identifying selected interacting domains that modulate protein
 PT interactions, or for preventing or treating metabolic disorders such as
 PT obesity or diabetes.

PS Claim 6; Page 173-174; 382pp; English.

The invention relates to a complex between two interacting proteins in
 adipocyte cells, given in the specification. The proteins are identified
 by selecting a bait protein from a known adipocyte marker and then
 performing a yeast 2-hybrid selection to isolate prey proteins encoded by
 members of an adipocyte cDNA library. The proteins are designated SID
 (STM) (selected interacting domains) proteins. Also included are a
 polynucleotide encoding a polypeptide in the adipocyte cells, a
 recombinant host cell expressing at least one of the interacting
 polypeptides of the complex, selecting a modulating compound in adipocyte
 cells, a SID (STM) polypeptide comprising any of the 738 amino acid
 sequences given in the specification (including its fragment or variant),
 a SID (STM) polynucleotide comprising any of the 738 nucleotide sequences
 given in the specification (including its fragment or variant), a vector
 comprising the SID (STM) polynucleotide, a recombinant host cell
 comprising the vector, a protein chip comprising the polypeptides and a
 record comprising all or part of the data, listed in the specification.
 The complex, polypeptides, polynucleotides and compounds are useful for
 preventing or treating metabolic disorders such as obesity or diabetes.
 The polynucleotides are useful as probes or primers. The complex is
 particularly useful for identifying selected interacting domains (SID
 (STM)) for screening drugs that modulate the protein interaction, thus
 exhibiting the therapeutic effect. The present sequence represents a SID
 (prey) protein of the invention

Sequence 244 AA;

Query Match 3.6%; Score 11; DB 6; Length 244;
 Best Local Similarity 100.0%; Pred. No. 0.082; 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
 Db 56 LAMNYLDRFLS 66
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RESULT 14

AAR27114
 ID AAR27114 standard; protein; 295 AA.

AC AAR27114;
 XX 25-MAR-2003 (revised)
 DT 20-MAY-1998 (first entry)
 XX
 DE pradi.

KW Cyclin; embryo; cdc2 protein kinase; parathyroid adenoma; G1;
 KW 11q13/11p15; oncogene; cell cycle regulation.

OS Homo sapiens.
 XX WO215603-A1.
 PN
 PD 17-SEP-1992.

XX 11-MAR-1992; 92WO-US001925.
 XX 11-MAR-1991; 91US-00667711.
 PR
 PA (GEO) GEN HOSPITAL CORP.

XX Arnold A;
 PI
 XX WPI; 1992-331664/40.
 DR N-PSDB; AAQ28889.

PT Prad1 cyclin and DNA encoding it - useful in promoting wound healing,
 PT and for diagnosing and treating cancer.
 XX
 PS Claim 1; Fig 6; 54pp; English.

CC The sequence given is a novel cyclin, pradi. Cyclins are a class of
 CC eukaryotic proteins which are identified by their cyclic accumulation and
 CC destruction at defined points in embryonic cell cycles. They bind to, and
 CC are essential for activation of, cdc2 protein kinase. The PRAD1 mRNA
 CC sequence was isolated from cells of a benign parathyroid adenoma. The
 CC gene was found to map to the 11q13 region and was found to be
 CC overexpressed in those parathyroid adenomas which had a 11q13/11p15
 CC chromosomal rearrangement. The PRAD locus is amplified and expressed in
 CC many squamous cells and mammary carcinomas. PRAD1 is thought to be an
 CC oncogene which figures in a variety of types of neoplasms. PRAD1 mRNA is
 CC highly conserved across species. PRAD1 mRNA levels fluctuate across the
 CC cell cycle, consistent with, but not proving a role in cell cycle
 CC regulation. The peak in PRAD1 mRNA levels occurs late in the cell cycle
 CC or in G1. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 295 AA;

Query Match 3.6%; Score 11; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 0.097;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
 Db 80 LAMNYLDRFLS 90
 |||||

RESULT 15

AAR29310

ID AAR29310 standard; protein; 295 AA.

AC AAR29310;
 XX 25-MAR-2003 (revised)
 DT 22-APR-1993 (first entry)
 XX
 DE Cyclin D1 protein.

XX Clone; pCYCD1-H12; mutant; yeast; strain; CLN; cyclin; gene; CLN 1;
 KW CLN 2; human; glioblastoma; cDNA library; expression vector; PADNS;
 KW transformant; pCYCD1-21; pCYCD1-19; HeLa.

OS Homo sapiens.
 XX WO9220796-A2.
 PN
 PD 26-NOV-1992.

XX 18-MAY-1992; 92WO-US004146.
 XX 16-MAY-1991; 91US-00701514.
 PR

XX (COLD-) COLD SPRING HARBOR LAB.
 PA
 PI Beach DH;

XX WPI; 1992-415774/50.
 DR N-PSDB; AAQ31873.

XX Recombinant mammalian D-type cyclin - replaces a CLN-type protein
 PT essential for cell start in budding yeast, its antibodies and probes
 PT being useful in detecting D-type cyclin in biological samples.
 XX
 PS Claim 6; Fig 2; 75pp; English.

XX This sequence is encoded by the clone pCYCD1-H12. A mutant yeast strain
 CC in which two of the three CLN cyclin genes (CLN 1 and CLN 2) were
 CC inactivate and expression of the third was conditional, was used to
 CC identify human cDNA clones that rescue yeast from CLN deficiency. A human
 CC glioblastoma cDNA library carried in a yeast expression vector (PADNS)
 CC was introduced into a mutant yeast strain. Two yeast transformants
 CC (pCYCD1-21 and pCYCD1-19) which grew despite the lack of function of all
 CC three CLN genes and were not revertants, were identified and recovered in
 CC E. coli. These two clones were shown to be independent clone representing
 CC the same gene. A HeLa cDNA library was screened for a full length cDNA
 CC clone using the 1.2 kb insert of pCYCD1-21 as a probe. The sequence
 CC isolated by this method was pCYCD1-H12. This protein has a molecular
 CC weight of approx. 34,000 daltons. Degenerate probes and primers were
 CC designed using the D1 gene sequence. These primers and probes were used
 CC in the isolation of the cyclin D2 and D3 genes. See also AAR29311-12.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 295 AA;

Query Match 3.6%; Score 11; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 0.097;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
 Db 80 LAMNYLDRFLS 90
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Search completed: March 23, 2004, 16:46:28
 Job time : 63 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 16:45:23 ; Search time 24 Seconds

(without alignments)
662.533 Million cell updates/sec

Title: US-09-530-209A-2

Perfect score: 308

Sequence: 1 MAEENELSLCTESNVDE.....SACCFSTKTHSSSYTHLS 308

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
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- 5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	4.2	335	4 US-09-404-296B-28	Sequence 28, Appl
2	13	4.2	354	4 US-09-404-296B-2	Sequence 2, Appl
3	11	3.6	102	2 US-08-580-988A-23	Sequence 23, Appl
4	11	3.6	152	2 US-08-460-694-4	Sequence 4, Appl
5	11	3.6	152	3 US-08-460-744-4	Sequence 4, Appl
6	11	3.6	152	3 US-07-667-711B-4	Sequence 4, Appl
7	11	3.6	295	1 US-07-947-120-8	Sequence 8, Appl
8	11	3.6	295	1 US-08-472-893A-8	Sequence 8, Appl
9	11	3.6	295	2 US-08-460-694-2	Sequence 2, Appl
10	11	3.6	295	2 US-08-464-517-2	Sequence 2, Appl
11	11	3.6	295	2 US-08-464-517-19	Sequence 19, Appl
12	11	3.6	295	2 US-08-464-517-20	Sequence 20, Appl
13	11	3.6	295	2 US-08-246-361A-2	Sequence 19, Appl
14	11	3.6	295	2 US-08-246-361A-19	Sequence 19, Appl
15	11	3.6	295	2 US-08-246-361A-20	Sequence 20, Appl
16	11	3.6	295	3 US-08-463-772-2	Sequence 2, Appl
17	11	3.6	295	3 US-08-463-772-19	Sequence 19, Appl
18	11	3.6	295	3 US-08-463-772-20	Sequence 20, Appl
19	11	3.6	295	3 US-08-460-744-2	Sequence 2, Appl
20	11	3.6	295	3 US-07-667-711B-2	Sequence 2, Appl
21	11	3.6	295	3 US-08-947-492-8	Sequence 8, Appl
22	11	3.6	295	5 PCT-US93-05000-2	Sequence 2, Appl
23	11	3.6	295	5 PCT-US93-05000-19	Sequence 19, Appl
24	11	3.6	295	5 PCT-US93-05000-20	Sequence 20, Appl
25	11	3.6	358	4 US-09-398-858-2	Sequence 2, Appl
26	11	3.6	358	4 US-09-398-858-12	Sequence 12, Appl
27	11	3.6	618	2 US-08-770-761A-3	Sequence 3, Appl

28	11	3.6	647	2 US-08-770-761A-8	Sequence 8, Appl
29	11	3.6	660	2 US-08-770-761A-2	Sequence 2, Appl
30	11	3.6	662	2 US-08-770-761A-5	Sequence 5, Appl
31	11	3.6	705	2 US-08-770-761A-7	Sequence 7, Appl
32	11	3.6	819	2 US-08-464-517-7	Sequence 7, Appl
33	11	3.6	819	2 US-08-246-361A-7	Sequence 7, Appl
34	11	3.6	819	3 US-08-463-772-7	Sequence 7, Appl
35	11	3.6	819	5 PCT-US93-05000-7	Sequence 7, Appl
36	10	3.2	189	2 US-08-464-517-21	Sequence 21, Appl
37	10	3.2	189	2 US-08-246-361A-21	Sequence 21, Appl
38	10	3.2	189	3 US-08-463-772-21	Sequence 21, Appl
39	10	3.2	189	5 PCT-US93-05000-21	Sequence 21, Appl
40	10	3.2	236	2 US-08-464-517-22	Sequence 22, Appl
41	10	3.2	236	2 US-08-246-361A-22	Sequence 22, Appl
42	10	3.2	236	3 US-08-463-772-22	Sequence 22, Appl
43	10	3.2	236	5 PCT-US93-05000-22	Sequence 22, Appl
44	10	3.2	289	2 US-08-246-361A-4	Sequence 4, Appl
45	10	3.2	289	5 PCT-US93-05000-4	Sequence 4, Appl

ALIGNMENTS

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RESULT 1
US-09-404-296B-28
; Sequence 28, Application US/09404296B
; Patent No. 6559358
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/09/404,296B
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-404-296B-28
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Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 124 QLAVACLSIAAK 136
Db 128 QLAVACLSIAAK 140
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RESULT 2
US-09-404-296B-2
; Sequence 2, Application US/09404296B
; Patent No. 6559358
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/09/404,296B
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-404-296B-2
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Query Match 4.2%; Score 13; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 124 QLAVACLSIAAK 136
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Db 142 QILAVACTSLAAK 154

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RESULT 3
US-08-580-988A-23
; Sequence 23, Application US/08580988A
; Patent No. 5856161
; GENERAL INFORMATION:
; APPLICANT: Aggarwal et al.
; TITLE OF INVENTION: Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Dr. Benjamin A. Adler
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,988A
; FILING DATE: January 3, 1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D., J.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5/721CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION:
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-580-988A-23

Query Match 3.6%; Score 11; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYIDRFLS 111
Db 29 LAMNYIDRFLS 39
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; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,694
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McConachy, Evelyn H.
; REGISTRATION NUMBER: 35,279
; REFERENCE/DOCKET NUMBER: 0609.4070002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2500
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-460-694-4

Query Match 3.6%; Score 11; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYIDRFLS 111
Db 25 LAMNYIDRFLS 35

RESULT 5
US-08-460-744-4
; Sequence 4, Application US/08460744
; Patent No. 6107541
; GENERAL INFORMATION:
; APPLICANT: Arnold, Andrew
; TITLE OF INVENTION: PRAD1 Cyclin and its cDNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,744
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McConachy, Evelyn H.
; REGISTRATION NUMBER: 35,279
; REFERENCE/DOCKET NUMBER: 0609.4070005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
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TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-744-4

Query Match 3.6%; Score 11; DB 3; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANNYLDRFLS 111
DB 25 LANNYLDRFLS 35

RESULT 6
US-07-667-711B-4

; Sequence 4, Application US/07667711B
; Patent No. 610700
; GENERAL INFORMATION:
; APPLICANT: ARNOLD, ANDREW
; TITLE OF INVENTION: Pradi Cyclin and Its CDNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/667, 711B
; FILING DATE: 11-MAR-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MCPHAIL, DONALD R.
; REGISTRATION NUMBER: 35,811
; REFERENCE/DOCKET NUMBER: 0609.4070000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-07-667-711B-4

Query Match 3.6%; Score 11; DB 3; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANNYLDRFLS 111
DB 25 LANNYLDRFLS 35

RESULT 7
US-07-947-120-8

; Sequence 8, Application US/07947120
; Patent No. 5538846
; GENERAL INFORMATION:
; APPLICANT: Meeker, Timothy C.
; TITLE OF INVENTION: BCL-1 Locus Nucleic Acid Probes and
; TITLE OF INVENTION: Assay Methods
; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: Steuart Street Tower, 18th Fl., One Market
; STREET: Plaza
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/947,120
; FILING DATE: 19920917
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.

; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: 91-210-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-777-9257

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 295 amino acids
; TYPE: AMINO ACID

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-947-120-8

Query Match 3.6%; Score 11; DB 1; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANNYLDRFLS 111
DB 80 LANNYLDRFLS 90

RESULT 8

; Sequence 8, Application US/08472893A
; Patent No. 5677130
; GENERAL INFORMATION:
; APPLICANT: Meeker, Timothy C.
; TITLE OF INVENTION: BCL-1 Locus Nucleic Acid Probes and
; TITLE OF INVENTION: Assay Methods
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: Steuart Street Tower, 18th Fl., One Market
; STREET: Plaza
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,893A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/947,120
; FILING DATE: 17-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863

REFERENCE/DOCKET NUMBER: 91-210-1
TELEPHONE: 415-777-9257
TELEFAX: 415-543-4219
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-893A-8

Query Match 3.6%; Score 11; DB 1; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
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Db 80 LAMNYLDRFLS 90

RESULT 9
US-08-460-694-2
Sequence 2, Application US/08460694
Patent No. 5858655
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McConachy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609,4070002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-460-694-2

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
|||
Db 80 LAMNYLDRFLS 90

RESULT 10
US-08-464-517-2
Sequence 2, Application US/08464517
Patent No. 5869640

GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHYE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-517-2

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
|||
Db 80 LAMNYLDRFLS 90

RESULT 11
US-08-464-517-19
Sequence 19, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHYE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,517
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-517-19

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
DB 80 LAMNYLDRFLS 90

RESULT 12
US-08-464-517-20
Sequence 20, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-004C
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-517-20

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
DB 80 LAMNYLDRFLS 90

RESULT 13
US-08-246-361A-2
Sequence 2, Application US/08246361A
Patent No. 5398582
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-246-361A-2

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111

Db 80 LANVYIDRFLS 90

RESULT 14
US-08-246-361A-19
; Sequence 19, Application US/08246361A
; Patent No. 5998582
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/246,361A
; FILING DATE: 19-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,514
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew P. Vincent
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIT-004C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 295 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-246-361A-19

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANVYIDRFLS 111
Db 80 LANVYIDRFLS 90

RESULT 15
US-08-246-361A-20
; Sequence 20, Application US/08246361A
; Patent No. 5998582
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/246,361A
; FILING DATE: 19-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,514
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew P. Vincent
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIT-004C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 295 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-246-361A-20

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANVYIDRFLS 111
Db 80 LANVYIDRFLS 90

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OM protein - protein search, using sw model

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Title: US-09-530-209a-2

Perfect score: 308

Sequence: 1 MAEENLESLICTESNVDF.....SACGFSFKTHDSSSYTHLS 308

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	4.2	354	15	US-10-388-269-2
2	12	3.9	349	15	US-10-310-154-426
3	11	3.6	36	14	US-10-199-820-241
4	11	3.6	129	12	US-10-424-599-183334
5	11	3.6	276	15	US-10-116-275-114
6	11	3.6	295	15	US-10-295-027-636
7	11	3.6	323	12	US-10-425-114-38749
8	11	3.6	358	14	US-10-320-230-2
9	11	3.6	358	14	US-10-320-230-12
10	11	3.6	358	15	US-10-409-701-5
11	11	3.6	385	15	US-10-264-049-2598
12	10	3.2	254	9	US-09-778-927A-53
13	10	3.2	289	9	US-09-919-497-54
14	10	3.2	289	13	US-10-024-066-2
15	10	3.2	289	13	US-10-024-066-4

16	10	3.2	349	12	US-10-424-599-178576
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18	10	3.2	383	12	US-10-424-599-282528
19	10	3.2	427	12	US-10-425-114-38905
20	9	2.9	182	12	US-10-424-599-239678
21	9	2.9	185	12	US-10-424-599-225086
22	9	2.9	238	12	US-10-424-599-273603
23	9	2.9	251	12	US-10-424-599-273602
24	9	2.9	271	12	US-10-424-599-253479
25	9	2.9	309	12	US-10-424-599-218205
26	9	2.9	315	15	US-10-388-269-8
27	9	2.9	340	12	US-10-425-114-49308
28	9	2.9	345	12	US-10-425-114-53407
29	9	2.9	345	12	US-10-425-114-56929
30	9	2.9	351	12	US-10-424-599-187289
31	9	2.9	383	12	US-10-425-114-53864
32	9	2.9	389	12	US-10-425-114-57533
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34	8	2.6	129	12	US-10-424-599-250717
35	8	2.6	212	15	US-10-369-493-4482
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39	8	2.6	229	12	US-10-424-599-226651
40	8	2.6	242	15	US-10-094-749-2076
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42	8	2.6	291	12	US-10-282-122A-49584
43	8	2.6	292	15	US-10-116-275-275
44	8	2.6	300	14	US-10-141-531-75
45	8	2.6	300	14	US-10-306-292-7

ALIGNMENTS

RESULT 1
US-10-388-269-2
Sequence 2, Appl
Publication No. US2003022122A1
GENERAL INFORMATION:
APPLICANT: MURRAY, James Augustus Henry
TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
FILE REFERENCE: 2121-0151P
CURRENT APPLICATION NUMBER: US/10/388, 269
CURRENT FILING DATE: 2003-03-12
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 354
TYPE: PRT
ORGANISM: Nicotiana tabacum
US-10-388-269-2

Query Match 4.2%; Score 13; DB 15; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.00078;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Or 124 QLAVALCISLAAK 136
Db 142 QLAVALCISLAAK 154
RESULT 2
US-10-310-154-426
Sequence 426, Application US/10310154
Publication No. US20030233670A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
APPLICANT: Chomel, Paul S.
APPLICANT: Adams, Thomas H
APPLICANT: Ruff, Thomas G.
APPLICANT: Agarwal, Ameeta K.
APPLICANT: Ahrens, Jeffrey E.

```
APPLICANT: Ball, James A.
APPLICANT: Banu, G.
APPLICANT: Bell, Erin
APPLICANT: Boddupalli, Raghava
APPLICANT: Deikman, Jill
APPLICANT: Deng, Molian
APPLICANT: Dong, Jinzhao
APPLICANT: Duff, Stephen M.
APPLICANT: Galligan, Meghan M.
APPLICANT: Hinchey, Brenda S.
APPLICANT: Huang, Shihshien
APPLICANT: Johnson, G. Richard
APPLICANT: Jung, Vincent
APPLICANT: Kretzmer, Keith A.
APPLICANT: Laccetti, Lucille B.
APPLICANT: Lai, Chao-Qiang
APPLICANT: Lee, Gary
APPLICANT: Lin, Jie-Yi
APPLICANT: Liu, Jinding
APPLICANT: Luethy, Michael M.
APPLICANT: Lund, Adrian
APPLICANT: Madson, Linda L.
APPLICANT: Malloy, Kathleen A.
APPLICANT: McKiel, Christine L.
APPLICANT: Miller, Philip W.
APPLICANT: Padmavathi, Manohikanti
APPLICANT: Parnell, Laurence D.
APPLICANT: Start, William G.
APPLICANT: Temmeesen, Dan
APPLICANT: Vidya, K.R.
APPLICANT: Wang, Haiyun
APPLICANT: Xin, Zhanqun
APPLICANT: Xu, Nanfei
APPLICANT: Yang, Chunzhi
APPLICANT: Zhang, Xiaoping
APPLICANT: Zhang, Qiang
APPLICANT: Zhao, Yajuan
APPLICANT: Zhou, Li
TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
FILE REFERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 426
LENGTH: 349
TYPE: PRT
ORGANISM: Zea mays
US-10-310-154-426

Query Match      3.9%; Score 12; DB 15; Length 349;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      125 LLAVACLSIAAK 136
DB      150 LLAVACLSIAAK 161

RESULT 3
US-10-199-820-241
Sequence 241, Application US/10199820
Publication No. US20030180739A1
GENERAL INFORMATION:
APPLICANT: Board of Trustees of the University of Illinois
APPLICANT: Primiano, Thomas
APPLICANT: Chang, Bey-dih
APPLICANT: Robinson, Igor
TITLE OF INVENTION: Methods and Reagents for Identifying Gene Targets for Treating Ca
FILE REFERENCE: 99,216-U
CURRENT APPLICATION NUMBER: US/10/199,820
```

```
CURRENT FILING DATE: 2002-09-23
NUMBER OF SEQ ID NOS: 314
SOFTWARE: PatentIn version 3.0
SEQ ID NO 241
LENGTH: 36
TYPE: PRT
ORGANISM: Homo sapiens
US-10-199-820-241

Query Match      3.6%; Score 11; DB 14; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      101 LAMNYIDRPLS 111
DB      25 LAMNYIDRPLS 35

RESULT 4
US-10-424-599-183234
Sequence 183234, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhao, Yinhua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 183234
LENGTH: 129
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_136474C.1.pcp
US-10-424-599-183234

Query Match      3.6%; Score 11; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      218 GIDFLFRPSE 228
DB      9 GIDFLFRPSE 19

RESULT 5
US-10-116-275-114
Sequence 114, Application US/10116275
Publication No. US20030211476A1
GENERAL INFORMATION:
APPLICANT: Elan Pharmaceutical Technology
APPLICANT: O'Mahony, Daniel J.
APPLICANT: Brayden, David
APPLICANT: Byrne, Daragh
APPLICANT: Lambkin, Imelda
APPLICANT: Higgins, Lisa
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
FILE REFERENCE: E1067/20087
CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOFTWARE: PatentIn version 3.1
SEQ ID NO 114
LENGTH: 276
TYPE: PRT
ORGANISM: Homo sapiens
US-10-116-275-114
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Query Match 3.6%; Score 11; DB 15; Length 276;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 LAMNYIDRFLS 111
Db 80 LAMNYIDRFLS 90

RESULT 6

US-10-295-027-636
; Sequence 636, Application US/10295027
; Publication No. US2003023350A1
; GENERAL INFORMATION:

; APPLICANT: Afari, Daniel
; APPLICANT: Aziz, Natsaba
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevez, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 636
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-636

Query Match 3.6%; Score 11; DB 15; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 LAMNYIDRFLS 111
Db 80 LAMNYIDRFLS 90

RESULT 7

US-10-425-114-38749
; Sequence 38749, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO: 38749
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73363C10_F11.pap
US-10-425-114-38749

Query Match 3.6%; Score 11; DB 12; Length 323;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 QLAVACLSLA 134
Db 113 QLAVACLSLA 123

RESULT 8

US-10-320-230-2
; Sequence 2, Application US/10320230
; Publication No. US20030110529A1
; GENERAL INFORMATION:
; APPLICANT: Lowe, Keith S.
; APPLICANT: Tao, Yumin
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Gregory, Carolyn A.
; APPLICANT: McElvett, John A.
; APPLICANT: Hoerster, George J.
; TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides
; TITLE OF INVENTION: and Methods of Use
; FILE REFERENCE: 0926D
; CURRENT APPLICATION NUMBER: US/10/320,230
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/101,551
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 09/398,858
; PRIOR FILING DATE: 1999-09-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 2
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Zea mays
US-10-320-230-2

Query Match 3.6%; Score 11; DB 14; Length 358;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 QLAVACLSLA 134
Db 148 QLAVACLSLA 158

RESULT 9

US-10-320-230-12
; Sequence 12, Application US/10320230
; Publication No. US20030110529A1
; GENERAL INFORMATION:
; APPLICANT: Lowe, Keith S.
; APPLICANT: Tao, Yumin

APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gregory, Carolyn A.
APPLICANT: McElvey, John A.
APPLICANT: Hoester, George J.
TITLE OF INVENTION: Cycloin D Polynucleotides, Polypeptides
TITLE OF INVENTION: and Methods of Use
FILE REFERENCE: 0926D
CURRENT APPLICATION NUMBER: US/10/320,230
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: 60/101,551
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 09/398,858
PRIOR FILING DATE: 1999-09-20
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 358
TYPE: PRT
ORGANISM: Zea mays
US-10-320-230-12

Query Match 3.6%; Score 11; DB 14; Length 358;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QLLAVACTSLA 134
Db 148 QLLAVACTSLA 158

RESULT 10
US-10-409-701-5
Sequence 5; Application US/10409701
Publication No. US20030221224A1
GENERAL INFORMATION:
APPLICANT: Zinselmeier, Chris
APPLICANT: Helentjaris, Timothy G.
TITLE OF INVENTION: Enhanced Silk Excretion Under Stress
FILE REFERENCE: 1421
CURRENT APPLICATION NUMBER: US/10/409,701
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: US 60/370,796
PRIOR FILING DATE: 2002-04-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 358
TYPE: PRT
ORGANISM: Zea mays
US-10-409-701-5

Query Match 3.6%; Score 11; DB 15; Length 358;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QLLAVACTSLA 134
Db 148 QLLAVACTSLA 158

RESULT 11
US-10-264-049-2598
Sequence 2598; Application US/10264049
Publication No. US20040005579A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA133PI
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467

PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patent In Ver. 3.1
SEQ ID NO 2598
LENGTH: 385
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (2)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (5)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-2598

Query Match 3.6%; Score 11; DB 15; Length 385;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRLS 111
Db 170 LAMNYLDRLS 180

RESULT 12
US-09-778-927A-53
Sequence 53; Application US/09778927A
Patent No. US2002068342A1
GENERAL INFORMATION:
APPLICANT: KHOSRAVI, Rami et al.
TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
FILE REFERENCE: 2786-0160P
CURRENT APPLICATION NUMBER: US/09/778,927A
CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: IL 134453
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: IL135341
PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 53
LENGTH: 254
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(254)
OTHER INFORMATION: Xaa = any amino acid, unknown, or other
US-09-778-927A-53

Query Match 3.2%; Score 10; DB 9; Length 254;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRL 110
Db 79 LAMNYLDRL 88

RESULT 13
US-09-919-497-54
Sequence 54; Application US/09919497
Patent No. US2002010662A1
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735

PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.0
SEQ ID NO 54
LENGTH: 289
TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-497-54

Query Match

Best Local Similarity 3.2%; Score 10; DB 9; Length 289;
Matches 10; Conservative 100.0%; Pred. No. 0.51; Mismatches 0; Indels 0; Gaps 0;

Qy 101 LAMNYLDRFL 110
Db 79 LAMNYLDRFL 88

RESULT 14

US-10-024-066-2
Sequence 2, Application US/10024066
Publication No. US20020166134A1
GENERAL INFORMATION:
APPLICANT: Field, Loren J.
APPLICANT: Pasumarthi, Kishore Babu S.
TITLE OF INVENTION: CARDIOMYOCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
FILE REFERENCE: 7037-450
CURRENT APPLICATION NUMBER: US/10/024,066
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/139,942
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: PCT/US00/16827
PRIOR FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 289
TYPE: PRT
ORGANISM: Mus musculus
US-10-024-066-2

Query Match 3.2%; Score 10; DB 13; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.51; Mismatches 0; Indels 0; Gaps 0;

Qy 101 LAMNYLDRFL 110
Db 78 LAMNYLDRFL 87

RESULT 15

US-10-024-066-4
Sequence 4, Application US/10024066
Publication No. US20020166134A1
GENERAL INFORMATION:
APPLICANT: Field, Loren J.
APPLICANT: Pasumarthi, Kishore Babu S.
TITLE OF INVENTION: CARDIOMYOCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
FILE REFERENCE: 7037-450
CURRENT APPLICATION NUMBER: US/10/024,066
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/139,942
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: PCT/US00/16827
PRIOR FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 289
TYPE: PRT
ORGANISM: Homo sapiens

US-10-024-066-4

Query Match 3.2%; Score 10; DB 13; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.51; Mismatches 0; Indels 0; Gaps 0;

Qy 101 LAMNYLDRFL 110
Db 79 LAMNYLDRFL 88

Search completed: March 23, 2004, 16:53:55
Job time : 53 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 23, 2004, 16:44:27 ; Search time 21 Seconds

(without alignments)
1410.809 Million cell updates/sec

Title: US-09-530-209A-2

Sequence: 1 MARENLESLCTESNVDE.....SACCFKTHDSSSYTHLS 308

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	6.5	317	2	T49995 cyclin protein-lik
2	13	4.2	334	2	S51650 cyclin delta-1 - A
3	13	4.2	339	2	A96725 hypothetical prote
4	12	3.9	291	2	S57922 cyclin D1 - Africa
5	12	3.9	291	2	S62730 cyclin D1 - zebra
6	11	3.6	295	2	A38977 cyclin D1 - human
7	11	3.6	295	2	A56523 cyclin D1 - mouse
8	11	3.6	295	2	JC2342 cyclin D1 - rat
9	11	3.6	418	2	S11678 cyclin A - African
10	10	3.2	288	2	JC4011 cyclin D2 - rat
11	10	3.2	288	2	I58372 cyclin D2 - mouse
12	10	3.2	289	2	A41984 cyclin D2 - human
13	10	3.2	289	2	A42822 cyclin D2 - mouse
14	10	3.2	291	2	JC4579 cyclin D2 - chick
15	9	2.9	291	2	S57925 cyclin D2 - Africa
16	9	2.9	321	2	T04720 hypothetical prote
17	9	2.9	372	2	T09961 cyclin D-like prot
18	9	2.9	376	2	T05420 cyclin delta-3 - A
19	8	2.6	178	2	T28045 hypothetical prote
20	8	2.6	237	2	C40035 cyclin-like protei
21	8	2.6	263	2	T00397 hypothetical prote
22	8	2.6	292	2	B42822 cyclin D3 - human
23	8	2.6	293	2	JC4012 cyclin D3 - rat
24	8	2.6	300	1	A69444 chlorodoxin-disulf
25	8	2.6	302	2	E85041 probable D-type cy
26	8	2.6	318	1	D23766 nodulation protein
27	8	2.6	328	2	B83261 hypothetical, prote
28	8	2.6	361	2	C84613 probable cyclin D
29	8	2.6	361	2	T45860 cyclin D3-like pro

30	8	2.6	383	2	S51651 cyclin delta-2 - A
31	8	2.6	501	2	T48336 hypothetical prote
32	8	2.6	509	2	S74935 hypothetical prote
33	8	2.6	542	2	S07386 55K protein precu
34	8	2.6	542	2	T35938 probable substrate
35	8	2.6	1383	2	T06091 hypothetical prote
36	8	2.6	1468	2	F70466 RNA polymerase bet
37	7	2.3	62	2	S45295 cyclin Cyc3 - Arab
38	7	2.3	93	2	T01876 hypothetical prote
39	7	2.3	102	2	T35134 hypothetical prote
40	7	2.3	137	2	S03489 T-cell receptor be
41	7	2.3	150	2	G87590 cyclochrome c-type
42	7	2.3	158	2	S61853 hnpk protein - Pse
43	7	2.3	159	2	T04297 hypothetical prote
44	7	2.3	166	2	D75173 hypothetical prote
45	7	2.3	201	1	T29447 probable bacitraci

ALIGNMENTS

RESULT 1
T49995
cyclin protein-lik - Arabidopsis thaliana

N:Alternate names: protein F12B17.210

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

C:Accession: T49995

R:Bevan, M.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.

submitted to the Protein Sequence Database, April 2000

A:Reference number: 225026

A:Accession: T49995

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-317 <BEV>

A:Cross-references: EMBL:AL353995; GSPDB:GN00063; ATSP:F12B17.210

A:Experimental source: cultivar Columbia; BAC clone F12B17

C:Genetics:

A:Gene: ATSP:F12B17.210

A:Map position: 5

A:Introns: 78/3; 107/3; 140/3; 221/3; 266/3

Query Match

Best Local Similarity 100.0%; Pred. No. 3.2e-12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 100 CIANNYIDRFSLVHDLPSGK 119

Db 91 CIANNYIDRFSLVHDLPSGK 110

RESULT 2

S51650

cyclin delta-1 - Arabidopsis thaliana

N:Alternate names: cyclin D homolog

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Sep-1997

C:Accession: S51650

R:Son, R.; Carmichael, J.P.; Shah, Z.H.; Murray, J.A.H.

submitted to the EMBL Data Library, December 1994

A:Description: A family of cyclin D homologs from plants differentially controlled by 9

A:Reference number: S51650

A:Molecule type: mRNA

A:Residues: 1-334 <SON>

A:Cross-references: EMBL:X83369; NID:G603504; PID:G603505

C:Keywords: cell cycle control; cell division control

Query Match

Best Local Similarity 100.0%; Pred. No. 5.2e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 124 QILAVACISLAK 136

Db 128 QLAVALCTSLAAK 140

RESULT 3

hypothetical protein F20P5.7 [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C/Accession: A96725
 R/Rheologs, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 anson, N.F.; Hughes, B.; Hutzar, L.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Liu, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.W.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: A96725
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-339 <STO>
 A/Cross-references: GB:AE005173; NID:92194121, PIDN:AA61096.1, GSPDB:GN00141
 C/Genetics:
 A/Gene: F20P5.7
 A/Map position: 1

Query Match 4.2%; Score 13; DB 2; Length 339;
 Best Local Similarity 100.0%; Pred. No. 5.3e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 QLAVALCTSLAAK 136
 128 QLAVALCTSLAAK 140

RESULT 4

cyclin D1 - African clawed frog
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 16-Jul-1999
 C/Accession: S57922
 R/Cockerill, M.J.; Hunt, T.
 submitted to the EMBL Data Library, July 1995
 A/Description: D-type cyclins in Xenopus laevis.
 A/Reference number: S57922
 A/Accession: S57922
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-291 <COC>
 A/Cross-references: EMBL:X89475; NID:9897818; PIDN:CAA61664.1; PID:9897819
 C/Superfamily: cyclin
 C/Keywords: cell cycle control

Query Match 3.9%; Score 12; DB 2; Length 291;
 Best Local Similarity 100.0%; Pred. No. 0.00049;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 LAMNYLDRFLSV 112
 78 LAMNYLDRFLSV 89

RESULT 5

cyclin D1 - zebra fish
 C/Species: Brachydanio rerio (zebra fish)
 C/Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
 C/Accession: S62730
 R/Yarden, A.; Salomon, D.; Geiger, B.

Biochim. Biophys. Acta 1264, 257-260, 1995
 A/Title: Zebrafish cyclin D1 is differentially expressed during early embryogenesis.
 A/Reference number: S62730; MUID:96138542; PMID:8547308
 A/Accession: S62730
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-291 <YAR>
 A/Cross-references: EMBL:X87581; NID:91143440; PIDN:CAA60885.1; PID:91143441
 C/Note: the source is designated as Danio rerio
 C/Superfamily: cyclin

Query Match 3.9%; Score 12; DB 2; Length 291;
 Best Local Similarity 100.0%; Pred. No. 0.00049;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 LAMNYLDRFLSV 112
 Db 80 LAMNYLDRFLSV 91

RESULT 6

cyclin D1 - human
 N/Alternate names: cyclin BCL1; cyclin D; PRAD1; probable bcl-1 transforming protein
 C/Species: Homo sapiens (man)
 C/Date: 27-Mar-1996 #sequence_revision 12-Apr-1996 #text_change 16-Jul-1999
 C/Accession: A38977; A41523; S14794; A40034; B40268; S51701; S54082; S34295
 R/Rimokh, R.; Berger, F.; Baetard, C.; Klein, B.; French, M.; Archimbaud, E.; Rouault,
 Blood 83, 3689-3696, 1994
 A/Title: Rearrangement of CCND1 (BCL1/PRAD1) 3' untranslated region in mantle-cell lymphoma.
 A/Reference number: A38977; MUID:94264323; PMID:8204893
 A/Accession: A38977
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-295 <RIM>
 A/Cross-references: GB:Z23022; NID:9312911; PIDN:CAA60558.1; PID:9312912
 R/Witthers, D.A.; Harvey, R.C.; Faust, J.B.; Melnyk, O.; Carey, K.; Meeker, T.C.
 Mol. Cell. Biol. 11, 4846-4853, 1991
 A/Title: Characterization of a candidate bcl-1 gene.
 A/Reference number: A41523; MUID:92017758; PMID:1833629
 A/Accession: A41523
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-295 <WIT>
 A/Cross-references: GB:M73554; NID:9179364; PIDN:AA58392.1; PID:9179365
 R/Motokura, T.; Bloom, T.; Kim, H.G.; Ueffner, H.; Ruderman, J.V.; Kronenberg, H.M.;
 Nature 350, 512-515, 1991
 A/Title: A novel cyclin encoded by a bcl1-linked candidate oncogene.
 A/Reference number: S14794; MUID:91194766; PMID:1826542
 A/Accession: S14794
 A/Molecule type: mRNA
 A/Residues: 1-295 <MOT>
 A/Cross-references: EMBL:X59798; NID:935631; PIDN:CAA42470.1; PID:935632
 R/Xiong, Y.; Connolly, T.; Fletcher, B.; Beach, D.
 Cell 65, 691-699, 1991
 A/Title: Human D-type cyclin.
 A/Reference number: A40034; MUID:91235304; PMID:1827756
 A/Accession: A40034
 A/Molecule type: mRNA
 A/Residues: 1-129; 'G', '131-187', 'S', '189-295 <XIO>
 A/Cross-references: GB:M64349; NID:9181244; PIDN:AA52136.1; PID:9181245
 A/Note: the authors translated the codon TCT for residue 188 as Leu
 R/Lew, D.J.; Dulic, V.; Reed, S.I.
 Cell 66, 1197-1206, 1991
 A/Title: Isolation of three novel human cyclins by rescue of G1 cyclin (Cln) function
 A/Reference number: A40268; MUID:92005671; PMID:1833066
 A/Accession: B40268
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-167; 'TA', '170-295 <LEW>
 A/Cross-references: GB:M74092
 R/Alberti, S.; Stella, M.; Dell'Arciprete, R.; Bucci, C.; Nutini, M.; Naglieri, A.M.;
 submitted to the EMBL Data Library, February 1994

A;Reference number: S51700
A;Accession: S51701
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 171-295 <ALB>
A;Cross-references: EMBL:X77754
R;Motoyura, T.; Arnold, A.
Genes Chromosomes Cancer 7, 89-95, 1993
A;Title: The PRAD1/cyclin D1 proto-oncogene: Genomic organization, 5' DNA sequence, and
A;Reference number: 154082; MUID:93326527; PMID:7687458
A;Accession: 154082
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-66 <RES>
A;Cross-references: GB:I09054; NID:g307344; PIDN:AAA36481.1; PID:g307345
C;Genetics:
A;Gene: GDB:CCND1; PRAD1; D11528
A;Cross-references: GDB:128222; OMIM:168461
A;Map position: 11q13.1-11q13.1
A;Note: this gene either contains or is contiguous to GDB:BCL1
C;Superfamily: cyclin
C;Keywords: cell cycle control; proto-oncogene

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred.No. 0.0053;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANMYLDRFLS 111
|||
Db 80 LANMYLDRFLS 90

RESULT 7
A;Accession: A56523
C;Species: Mus musculus (house mouse)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 16-Jul-1995
C;Accession: A56523; A40035
R;Smith, R.; Peters, G.; Dickson, C.
Genomics 25, 85-92, 1995
A;Title: Genomic organization of the mouse cyclin D1 gene (Cyl-1).
A;Reference number: A56523; MUID:95293413; PMID:7774959
A;Accession: A56523
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-295 <SLT>
A;Cross-references: GB:S78355; NID:g994896; PIDN:AA34495.1; PID:g994897
R;Matsumine, H.; Roussel, M.F.; Ashmun, R.A.; Sherr, C.J.
Cell 65, 701-713, 1991
A;Title: Colony-stimulating factor 1 regulates novel cyclins during the G1 phase of the
A;Reference number: A40035; MUID:91233305; PMID:1827757
A;Accession: A40035
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-295 <MAT>
A;Cross-references: GB:M64403; NID:g192877; PIDN:AAA37502.1; PID:g192878
C;Superfamily: cyclin
C;Keywords: cell cycle control

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred.No. 0.0053;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANMYLDRFLS 111
|||
Db 80 LANMYLDRFLS 90

RESULT 8
JC2342
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1995

C;Accession: JC2342; S44147
R;Bianchi, S.; Fabiani, S.; Muratori, M.; Arnold, A.; Sakaguchi, K.; Miki, T.; Brandi,
Biochem. Biophys. Res. Commun. 204, 691-700, 1994
A;Title: Calcium modulates the cyclin D1 expression in a rat parathyroid cell line.
A;Reference number: JC2342; MUID:95071382; PMID:7980531
A;Accession: JC2342
A;Molecule type: mRNA
A;Residues: 1-295 <BIA>
A;Cross-references: EMBL:X75207; NID:g473122; PIDN:CAA53020.1; PID:g473123
A;Experimental source: epithelial parathyroid cell line
R;Bianchi, S.; Fabiani, S.; Muratori, M.; Sakaguchi, K.; Arnold, A.; Miki, T.; Brandi,
submitted to the EMBL Data Library, September 1993
A;Description: Cloning and calcium regulation of cyclin D1 gene in a rat parathyroid c
A;Reference number: S44147
A;Accession: S44147
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-295 <B12>
A;Cross-references: EMBL:X75207; NID:g473122; PIDN:CAA53020.1; PID:g473123
C;Superfamily: cyclin
C;Keywords: cell cycle control

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred.No. 0.0053;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANMYLDRFLS 111
|||
Db 80 LANMYLDRFLS 90

RESULT 9
S11678
C;Species: Xenopus laevis (African clawed frog)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1995
C;Accession: S11678
R;Kishnall, J.; Goleteyn, R.; Hill, C.S.; Hunt, T.
EMBO J. 9, 2865-2875, 1990
A;Title: The A- and B-type cyclin associated cdc2 kinases in Xenopus turn on and off a
A;Reference number: S11678; MUID:90360999; PMID:2143983
A;Accession: S11678
A;Molecule type: mRNA
A;Residues: 1-418 <MIN>
A;Cross-references: EMBL:X53745; NID:g64644; PIDN:CAA37775.1; PID:g64645
C;Superfamily: cyclin
C;Keywords: cell cycle control

Query Match 3.6%; Score 11; DB 2; Length 418;
Best Local Similarity 100.0%; Pred.No. 0.0073;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANMYLDRFLS 111
|||
Db 220 LANMYLDRFLS 230

RESULT 10
JC4011
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Jun-2000
C;Accession: JC4011
R;Hosokawa, Y.; Ohga, T.; Nakashima, K.
Gene 147, 249-252, 1994
A;Title: Induction of D2 and D3 cyclin-encoding genes during promotion of the G1/S tra
A;Reference number: JC4011; MUID:95011623; PMID:7926809
A;Accession: JC4011
A;Molecule type: mRNA
A;Residues: 1-288 <HOS>
A;Cross-references: GB:D16308; NID:g577334; PIDN:BA03815.1; PID:g577335
A;Experimental source: Nb2 cell
A;Note: The authors translated the codon GAA for residue 68 as Glu, TGC for residue 104

C;Genetics:
A;Gene: d2
C;Superfamily: cyclin
C;Keywords: cell cycle control

Query Match 3.2%; Score 10; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFL 110
Db 78 LAMNYLDRFL 87

RESULT 11
158372
cyclin D2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: 158372

R;Hanna, Z.; Jankowski, M.; Tremblay, P.; Jiang, X.M.; Malatovich, A.; Francke, U.; Jolh
Oncogene 8, 1661-1666, 1993

A;Title: The VIN1 gene, identified by provirus insertional mutagenesis, is the cyclin D2
A;Reference number: 158372; PMID:93275661; PMID:8502486

A;Accession: 158372
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
A;Residues: 1-288 <RES>

A;Cross-references: GB:I09752; NID:g203703; PIDN:AAA41010.1; PID:g203704

C;Genetics:
A;Gene: VIN1
C;Superfamily: cyclin

C;Keywords: cell cycle control

Query Match 3.2%; Score 10; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFL 110
Db 78 LAMNYLDRFL 87

RESULT 12
A41984

cyclin D2 - mouse
N;Alternate names: cyclin-like protein Cy12

C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999

C;Accession: A41984; B40035
R;Kiyokawa, H.; Busquets, X.; Powell, C.T.; Ngo, L.; Rifkin, R.A.; Marks, P.A.

Proc. Natl. Acad. Sci. U.S.A. 89, 2444-2447, 1992

A;Title: Cloning of a D-type cyclin from murine erythroleukemia cells.
A;Reference number: A41984; PMID:92196134; PMID:1372445

A;Accession: A41984
A;Status: preliminary

A;Molecule type: mRNA
A;Residues: 1-289 <KTY>

A;Cross-references: GB:M63749; NID:G192938; PIDN:AAA37519.1; PID:G192939

A;Experimental source: erythroleukemia cells
A;Note: sequence inconsistent with the nucleotide translation

A;Note: sequence extracted from NCBI backbone (NCBIN:88492, NCBI:88493)
R;Matsumine, H.; Rousset, M.F.; Ashmun, R.A.; Sherr, C.J.

Cell 65, 701-713, 1991

A;Title: Colony-stimulating factor 1 regulates novel cyclins during the G1 phase of the
A;Reference number: A40035; PMID:91235305; PMID:1827757

A;Accession: B40035
A;Status: preliminary

A;Molecule type: mRNA
A;Residues: 54-289 <MAT>
A;Cross-references: GB:M66182
C;Superfamily: cyclin
C;Keywords: cell cycle control

Query Match 3.2%; Score 10; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFL 110
Db 78 LAMNYLDRFL 87

RESULT 13
A42822
cyclin D2 - human

C;Species: Homo sapiens (man)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999

C;Accession: A42822; 137268; A42821; S26580

R;Xiong, Y.; Menninger, J.; Beach, D.; Ward, D.C.

Genomics 13, 575-584, 1992

A;Title: Molecular cloning and chromosomal mapping of CCND genes encoding human D-type
A;Reference number: A42822; PMID:92347851; PMID:1386336

A;Accession: A42822
A;Molecule type: mRNA

A;Residues: 1-289 <XIO>
A;Cross-references: GB:M90813; NID:G179999; PIDN:AAA51926.1; PID:G180000

A;Note: sequence extracted from NCBI backbone (NCBIN:109683, NCBI:109685)
R;Palmero, I.; Holder, A.; Sinclair, A.J.; Dickson, C.; Peters, G.

Oncogene 8, 1049-1054, 1993

A;Title: Cyclins D1 and D2 are differentially expressed in human B-lymphoid cell lines
A;Reference number: 137268; PMID:93205384; PMID:8455931

A;Accession: 137268
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
A;Residues: 1-289 <RE2>

A;Cross-references: EMBL:X68452; NID:G38415; PIDN:CAA48493.1; PID:G38416

R;Inaba, T.; Matsushime, H.; Valentine, M.; Rousset, M.F.; Sherr, C.J.; Look, A.T.

Genomics 13, 565-574, 1992

A;Title: Genomic organization, chromosomal localization, and independent expression of
A;Reference number: A42821; PMID:92347850; PMID:1386335

A;Accession: A42821
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA
A;Residues: 1-165, 'NV', 168-223, 'H', 225-240 <RES>

A;Cross-references: GB:M88083; NID:G180008; PIDN:AAA51928.1; PID:G180010

C;Genetics:
A;Gene: GDB:CCND2

A;Cross-references: GDB:128968; OMIM:123833

A;Map position: 12p13-12p13
C;Superfamily: cyclin
C;Keywords: cell cycle control

Query Match 3.2%; Score 10; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFL 110
Db 79 LAMNYLDRFL 88

RESULT 14
JC4579
cyclin D2 - chicken

N;Alternate names: Cy1 D2
C;Species: Gallus gallus (chicken)

C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 31-Mar-2000
C;Accession: JC4579
R;Li, H.; Grenet, J.; Kidd, V.J.

Gene 167, 341-342, 1995

A;Title: Structure and gene expression of avian cyclin D2.
A;Reference number: JC4579; PMID:96144302; PMID:8566807

A;Accession: JC4579
A;Molecule type: mRNA
A;Residues: 1-291 <LIH>

A/Cross-references: GB:U28980; NID:g968968; PIDN:AA96955.1; PID:g968968
A/Experimental source: U93 T-cell
C/Comment: This protein acts as a regulator of the cell-cycle-dependent protein kinase gene product, binds to these products in a combinatorial fashion, activates their enzyme activity
C/Genetics:
A/Gene: cycl2
C/Superfamily: cyclin
C/Keywords: cell cycle control
F/29-193/Region: cyclin-box similarity

Query Match 3.2%; Score 10; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFL 110
|||||
DB 79 LAMNYLDRFL 88

RESULT 15

S57925
cyclin D2 - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 13-Jan-1996 #sequence_revision 12-Apr-1996 #ext_change 16-Jul-1999
C/Accession: S57925; S51681
R/Cockerill, M.J.; Hunt, T.
submitted to the EMBL Data Library, July 1995
A/Description: D-type cyclins in Xenopus laevis.
A/Reference number: S57922
A/Accession: S57925
A/Molecule type: mRNA
A/Residues: 1-291 <CDS>
A/Cross-references: EMBL:X89476; NID:g897820; PIDN:CAA61665.1; PID:g897821
R/Raib, F.; Jesus, C.
submitted to the EMBL Data Library, December 1994
A/Reference number: S51681
A/Accession: S51681
A/Molecule type: mRNA
A/Residues: 1-291 <RAI>
A/Cross-references: EMBL:X83503; NID:g603899; PIDN:CAA58493.1; PID:g603900
C/Superfamily: cyclin
C/Keywords: cell cycle control

Query Match 2.9%; Score 9; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 AMNYLDRFL 110
|||||
DB 80 AMNYLDRFL 88

Search completed: March 23, 2004, 16:48:29
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 23, 2004, 16:40:35 ; Search time 18 Seconds
(without alignments)
890.978 Million cell updates/sec

Title: US-09-530-209A-2

Perfect score: 308
Sequence: 1 MAEENIEISLCTESNVDE.....SACCFSEKTHDSSSYHLIS 308

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : SwissProt_42.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	4.2	335	1 CGD1_ARATH	P42751 arabidopsis
2	12	3.9	291	1 CGD1_BRARE	O90459 brachydanio
3	12	3.9	291	1 CGD1_XENLA	P50785 xenopus lae
4	11	3.6	292	1 CGD1_CHICK	P55189 gallus gall
5	11	3.6	295	1 CGD1_HUMAN	P24385 homo sapien
6	11	3.6	295	1 CGD1_MOUSE	P25342 mus musculu
7	11	3.6	295	1 CGD1_RAT	P39948 rattus norv
8	11	3.6	418	1 CGA1_XENLA	P18606 xenopus lae
9	10	3.2	288	1 CGD2_RAT	O04877 rattus norv
10	10	3.2	289	1 CGD2_HUMAN	P30279 homo sapien
11	10	3.2	289	1 CGD2_MOUSE	P30280 mus musculu
12	10	3.2	291	1 CGD2_CHICK	P49706 gallus gall
13	9	2.9	291	1 CGD2_XENLA	P53782 xenopus lae
14	9	2.9	376	1 CGD3_ARATH	P42753 arabidopsis
15	8	2.6	292	1 CGD3_HUMAN	P30281 homo sapien
16	8	2.6	292	1 CGD3_MOUSE	P30282 mus musculu
17	8	2.6	293	1 CGD3_RAT	P48961 rattus norv
18	8	2.6	318	1 NODD_RHILT	P04680 rhizobium 1
19	8	2.6	361	1 CGD2_ARATH	P42752 arabidopsis
20	8	2.6	382	1 CGB2_ORYZA	O94939 oryza sativ
21	8	2.6	391	1 CGA1_CARAU	O92161 carassius a
22	8	2.6	542	1 XP55_STRUT	P06109 streptomyce
23	8	2.6	1375	1 RPOB_COXBU	O87903 coxiella bu
24	8	2.6	1468	1 RPOB_AQVAE	O67762 aquifex aeo
25	7	2.3	104	1 GLRX_VERFO	O81187 vermicia fo
26	7	2.3	124	1 PHPI_MOUSE	O9d49 mus musculu
27	7	2.3	220	1 REHY_ORYSA	P52513 oryza sativ
28	7	2.3	233	1 B915_XENLA	P40745 xenopus lae
29	7	2.3	240	1 ATP7_ARATH	O95j12 arabidopsis
30	7	2.3	244	1 FIMB_BOKEP	P33409 bordetella
31	7	2.3	246	1 PHBB_CHWVI	P45335 chromatiunf
32	7	2.3	251	1 GLO2_BUCAI	P57336 buchnera ap
33	7	2.3	251	1 Y137_CHLPM	O92946 chlamydia p

34	7	2.3	253	1	UT11_MOUSE	O9czj1 mus musculu
35	7	2.3	277	1	THIG_SYNEL	O8dmp6 synecococc
36	7	2.3	279	1	MOVP_CMYIX	O66119 cucumber mo
37	7	2.3	309	1	PANC_MYCTU	O06280 mycobacteri
38	7	2.3	333	1	AMP_TMPBA	O24006 i antimicro
39	7	2.3	394	1	MPGS_AERPE	O9y4m5 aeropyrum p
40	7	2.3	395	1	Y063_SYNY3	O55147 synecocyst
41	7	2.3	424	1	CRIC_ORYSA	O95148 oryza sativ
42	7	2.3	428	1	CG2B_ARATH	P30183 arabidopsis
43	7	2.3	444	1	RBL_MATAN	P93936 watsonta an
44	7	2.3	462	1	ALB3_ARATH	O8lbp4 arabidopsis
45	7	2.3	467	1	ROCE_BACST	P39137 bacillus su

ALIGNMENTS

RESULT 1
CGD1_ARATH STANDARD; PRT; 335 AA.
AC P42751; O04525;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cyclin delta-1.
GN CYCD1 OR AT1G70210 OR F20P5.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta; TISSUE=Seedling;
RX MEDLINE=95210930; PubMed=7696881;
RA Soni R., Carmichael J.P., Shah Z.H., Murray J.A.H.;
RT "A family of cyclin D homologs from plants differentially controlled
RT by growth regulators and containing the conserved retinoblastoma
RT protein interaction motif."
RL Plant Cell 7:85-103 (1995).
RN [2]
RP REVISIONS.
RA Murray J.A.H.;
RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Becker U.R., Palm C.U., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Dunn M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gali J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremetskaia I., Kutz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani A.,
RA Maltischer J., Miranda M., Nguyen M., Nieman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.O., Tambunga G., Toriumi M.J., Town C.D.,
RA Utechtack T., Van Aken S., Vayberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Frazer C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana."
RL Nature 408:816-820 (2000).
RN [4]
RP SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.

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DR EMBL: X83369; CAA58285.1; -.
 DR EMBL: ACC02062; AAB61096.1; -.
 DR PIR: A96725; A96725.
 DR InterPro: IPR006670; Cyclin.
 DR InterPro: IPR004367; Cyclin_Cterm.
 DR InterPro: IPR006671; Cyclin_N.
 DR Pfam: PF00134; cyclin; 1.
 DR Pfam: PF02984; cyclin_C; 1.
 DR SMART: SM00385; CYCLIN; 1.
 DR PROSITE: PS00292; CYCLINS; 1.
 DR Cyclin; Cell cycle; Cell division; Multigene family.
 FT CONFLICT 313 313 S -> SPSSS (IN REF. 3).
 SQ SEQUENCE 335 AA; 37868 MW; D365673D2FC639 CRC64;

Query Match 4.2%; Score 13; DB 1; Length 335;
 Best Local Similarity 100.0%; Pred. No. 0.0001;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QLAVALCTIAAK 136
 DB 128 QLAVALCTIAAK 140

RESULT 2
 ID CGDI_BRARE STANDARD; PRT; 291 AA.
 AC Q90459;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE GI/S-specific cyclin D1.
 GN CCND1 OR CYCD1.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9613542; PubMed=8547308;
 RA Yarden A.; Salomon D.; Geiger B.;
 RT "Zebrafish cyclin D1 is differentially expressed during early
 embryogenesis";
 RU Biochim. Biophys. Acta 1264:257-260(1995).
 CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
 (start) transition.
 CC -1- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
 a serine/threonine kinase holoenzyme complex. The cyclin subunit
 impacts substrate specificity to the complex.
 CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.

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DR EMBL: X87581; CAA60885.1; -.
 DR PIR: S62730; S62730.
 DR ZFIN: ZDB-GENE-980526-176; ccnd1.
 DR InterPro: IPR006670; Cyclin.
 DR InterPro: IPR004367; Cyclin_Cterm.
 DR InterPro: IPR006671; Cyclin_N.
 DR Pfam: PF00134; cyclin; 1.
 DR Pfam: PF02984; cyclin_C; 1.
 DR SMART: SM00385; CYCLIN; 1.
 DR PROSITE: PS00292; CYCLINS; 1.

KW Cyclin; Cell cycle; Cell division.
 SQ SEQUENCE 291 AA; 33067 MW; FA5274CB1B46D5EF CRC64;

Query Match 3.9%; Score 12; DB 1; Length 291;
 Best Local Similarity 100.0%; Pred. No. 0.00084;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYIDREFLSV 112
 DB 80 LAMNYIDREFLSV 91

RESULT 3
 ID CGDI_XENLA STANDARD; PRT; 291 AA.
 AC P50755;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE GI/S-specific cyclin D1.
 GN CCND1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodidae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cockerill M.J.; Hunt T.;
 RU Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
 (start) transition.
 CC -1- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
 a serine/threonine kinase holoenzyme complex. The cyclin subunit
 impacts substrate specificity to the complex.
 CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.

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DR EMBL: X89475; CAA61664.1; -.
 DR PIR: S57922; S57922.
 DR InterPro: IPR006670; Cyclin.
 DR InterPro: IPR004367; Cyclin_Cterm.
 DR InterPro: IPR006671; Cyclin_N.
 DR Pfam: PF00134; cyclin; 1.
 DR Pfam: PF02984; cyclin_C; 1.
 DR SMART: SM00385; CYCLIN; 1.
 DR PROSITE: PS00292; CYCLINS; 1.
 KW Cyclin; Cell cycle; Cell division; Multigene family.
 SQ SEQUENCE 291 AA; 32953 MW; A4747C5BD1679087 CRC64;

Query Match 3.9%; Score 12; DB 1; Length 291;
 Best Local Similarity 100.0%; Pred. No. 0.00084;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYIDREFLSV 112
 DB 78 LAMNYIDREFLSV 89

RESULT 4
 ID CGDI_CHICK STANDARD; PRT; 292 AA.
 AC P55169;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE G1/S-specific cyclin D1.
 GN CCND1.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OK NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Li H., Lahti J.M., Kidd V.J.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
 CC (start) transition. Interacts with the CDK4 and CDK6 protein
 CC kinases (by similarity).
 CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
 CC -----
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 CC -----
 DR EMBL: U40844; AAA83271.1; -
 DR InterPro: IPR006670; Cyclin.
 DR InterPro: IPR004367; Cyclin_Cterm.
 DR InterPro: IPR006671; Cyclin_N.
 DR Pfam: PF00134; cyclin_1.
 DR Pfam: PF02984; cyclin_C; 1.
 DR SMART: SM00385; CYCLIN; 1.
 DR PROSITE: PS00292; CYCLINS; 1.
 DR PROSITE: PS00292; Cell division; Multigene family.
 KW CYCLIN; Cell cycle; Cell division; Multigene family.
 SQ SEQUENCE 292 AA; 33263 MW; 7B543029DB45A67D CRC64;
 Query Match 3.6%; Score 11; DB 1; Length 292;
 Best Local Similarity 100.0%; Pred. No. 0.0078;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 101 LAMNYLDRLPS 111
 DB 80 LAMNYLDRLPS 90
 CG1 HUMAN STANDARD; PRT; 295 AA.
 ID CGD1 HUMAN
 AC P24385;
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-OCT-2003 (Rel. 42, Last annotation update)
 DE G1/S-specific cyclin D1 (PRAD1 oncogene) (BC1-1 oncogene).
 GN CCND1 OR PRAD1 OR BCL1.
 OS Homo sapiens (human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91194766; PubMed=1826542;
 RA Motokura T., Bloom T., Kim H.G., Ueppner H., Ruderman J.V.,
 RA Kronenberg H.M., Arnold A.;
 RT "A novel cyclin encoded by a bcl1-linked candidate oncogene";
 RL Nature 350:512-515(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92005671; PubMed=1833066;
 RA Lew D.J., Dulic V., Reed S.I.;
 RT "Isolation of three novel human cyclins by rescue of G1 cyclin (Cln)
 RL function in yeast";
 RL Cell 66:1197-1206(1991).
 RP SEQUENCE FROM N.A.

RX MEDLINE=91235304; PubMed=1827756;
 RA Xiong Y., Connolly T., Fitchner B., Beach D.;
 RT "Human D-type cyclin";
 RL Cell 65:691-699(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=92017758; PubMed=1833629;
 RA Withers D.A., Harvey R.C., Faust J.B., Melnyk O., Carey K.,
 RA Wecker T.C.;
 RT "Characterization of a candidate bcl-1 gene";
 RL Mol. Cell. Biol. 11:4846-4853(1991).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94264323; PubMed=8204893;
 RA Rimokh R., Berger F., Bastard C., Klein B., French M., Archimbaud E.,
 RA Rouault J.-P., Santa Lucia B., Duret L., Vulliamme M.;
 RT "Rearrangement of CCND1 (BCL1/PRAD1) 3' untranslated region in
 RL mantle-cell lymphomas and t(11q13)-associated leukemias";
 RL Blood 83:3689-3696(1994).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Wittrik L.A., Nickerson D.A.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Helen F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hully S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP INTERACTION WITH CDK4 AND CDK6
 RX MEDLINE=94134440; PubMed=8302605;
 RA Bates S., Bonetto L., McAllian D., Parry D., Holder A., Dickson C.,
 RA Peters G.;
 RT "CDK6 (PLSTRB) and CDK4 (PSK-T3) are a distinct subset of the
 RL cyclin-dependent kinases that associate with cyclin D1";
 RL Oncogene 9:71-79(1994).
 CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
 CC (start) transition.
 CC -1- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
 CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
 CC impacts substrate specificity to the complex.
 CC -1- DISEASE: Involved in B-lymphocytic malignancy (particularly
 CC mantle-cell lymphoma (MCL)) by a chromosomal translocation
 CC t(11;14)(q13;q32) that involves CCND1 and immunoglobulin gene
 CC regions (BCL1 oncogene). Activation of CCND1 may be oncogenic by
 CC directly altering progression through the cell cycle.
 CC -1- DISEASE: Involved in a subset of parathyroid adenomas by a
 CC chromosomal translocation t(11;11)(q13;p15) that involves CCND1
 CC and the parathyroid hormone (PTH) enhancer (PRAD1 oncogene).
 CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
 CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/BCL1.html".

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CC -----
DR EMBL: X59798; CAA42470.1; -
DR EMBL: M74092; -; NOT ANNOTATED_CDS.
DR EMBL: M64349; AAA52136.1; -
DR EMBL: M73554; AAA58392.1; -
DR EMBL: Z23022; CAA80558.1; -
DR EMBL: AF511593; AAA43300.2; -
DR EMBL: BC000076; AAH00076.1; -
DR EMBL: BC001501; AAH01501.1; -
DR EMBL: BC014078; AAH14078.1; -
DR EMBL: BC023620; AAH23620.1; -
DR EMBL: BC025302; AAH25302.1; -
DR PIR: A38977; A38977.
DR Genew: HGNC:1582; CCND1.
DR GK: P24385; -
DR MTM: 151400; -
DR MTM: 168461; -
DR GO: GO:0000082; P:G1/S transition of mitotic cell cycle; NMS.
DR InterPro: IPR006670; Cyclin.
DR InterPro: IPR004367; Cyclin_Cterm.
DR InterPro: IPR006671; Cyclin_N.
DR Pfam: PF00134; cyclin_1.
DR Pfam: PF02984; cyclin_C_1.
DR SMART: SM00385; CYCLIN; 1.
DR PROSITE: PS00292; CYCLINS; 1.
DR Cyclin; Cell cycle; Cell division; Multigene family; Proto-oncogene;
KW Chromosomal translocation.
FT CONFLICT 130 130 N -> G (IN REF. 3).
FT CONFLICT 168 169 MP -> IA (IN REF. 2).
FT CONFLICT 188 188 L -> S (IN REF. 3).
SQ SEQUENCE 295 AA; 33729 MW; 3CC00C905F58D3A CRC64;

Query Match 3.6%; Score 11; DB 1; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
DB 80 LAMNYLDRFLS 90

RESULT 6
CGDI MOUSE STANDARD; PRT; 295 AA.
ID CGDI_MOUSE
AC P25322;
DT 01-MAY-1992 (Rel. 22; Created)
DT 01-MAY-1992 (Rel. 22; Last sequence update)
DT 15-MAR-2004 (Rel. 43; Last annotation update)
DE G1/S-specific cyclin D1.
DE GN CNBD1 OR CYL-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91235305; PubMed=1827757;
RX Macintosh H.; Rousset M.F.; Ahmun R.A.; Sherr C.J.;
RT "Colony-stimulating factor 1 regulates novel cyclins during the G1
RT phase of the cell cycle.";
RL Cell 65:701-713(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95293413; PubMed=7774959;
RX Smith R.; Peters G.; Dickson C.;

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RT "Genomic organization of the mouse cyclin D1 gene (Cyl-1).";
RL Genomics 25:85-92(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC SRRAIN=129; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Krausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shellen G.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Strapleno M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Usdin T.B.; Toehlyuk S.; Carninci P.; Prange C.;
RA Rana S.S.; Loquellano N.A.; Peters G.D.; Abramson R.D.; Mullaly S.J.;
RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
RA Richards S.; Morley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
RA Villalón D.K.; Muzny D.C.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Whiting J.; Helton E.; Ketteman M.; Madan A.; Rodriguez S.; Sanchez A.;
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;
RA Blakeley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;
RA Butcherfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smalins D.E.;
RA Schnerch A.; Schein J.E.; Jones S.J.M.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
CC (start) transition.
CC -1- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
CC impacts substrate specificity to the complex.
CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M64403; AAA37502.1; -
DR EMBL: S78355; AAB34495.1; -
DR EMBL: BC044841; AAR44841.1; -
DR PIR: A56523; A56523.
DR MGD: MGI:88313; Ccnd1.
DR GO: GO:0005829; C:cytosol; IDA.
DR GO: GO:0005634; C:nucleus; IDA.
DR GO: GO:0016538; F:cyclin-dependent protein kinase, intrinsic . . . IDA.
DR GO: GO:0045444; F:adipocyte differentiation; IDA.
DR GO: GO:0000320; P:re-entry into mitotic cell cycle; IDA.
DR InterPro: IPR006670; Cyclin.
DR InterPro: IPR004367; Cyclin_Cterm.
DR InterPro: IPR006671; Cyclin_N.
DR Pfam: PF00134; cyclin_1.
DR Pfam: PF02984; cyclin_C_1.
DR SMART: SM00385; CYCLIN; 2.
DR PROSITE: PS00292; CYCLINS; 1.
DR Cyclin; Cell cycle; Cell division; Multigene family.
KW Cyclin; Cell cycle; Cell division; Multigene family.
SQ SEQUENCE 295 AA; 33428 MW; 3A79736B4163251B CRC64;

Query Match 3.6%; Score 11; DB 1; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
DB 80 LAMNYLDRFLS 90

RESULT 7
CGDI RAT STANDARD; PRT; 295 AA.
ID CGDI_RAT

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AC P39948; (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE G1/S-specific cyclin D1.
GN CCND1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93330551; PubMed=8336937;
RA Tamura K., Kanaoka Y., Jinno S., Nagata A., Ogiso Y., Shimizu K.,
RA Hayakawa T., Nojima H., Okayama H.;
RT "Cyclin G: a new mammalian cyclin with homology to fission yeast
RT Cig1."
RL Oncogene 8:2113-2118(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95071382; PubMed=7980531;
RA Bianchi S., Fabiani S., Muratori M., Arnold A., Sakaguchi K., Miki T.,
RA Brandi M.L.;
RT "Calcium modulates the cyclin D1 expression in a rat parathyroid cell
RT line."
RL Biochem. Biophys. Res. Commun. 204:691-700(1994).
CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
CC (start) transition. Interacts with the CDK4 and CDK6 protein
CC kinases.
CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
CC
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CC
CC EMBL: D14014; BAA03115.1; -
CC EMBL: X75207; CAA53020.1; -
CC PIR: JC2342; JC2342.
CC InterPro: IPR006670; Cyclin.
CC InterPro: IPR004367; Cyclin_Cterm.
CC InterPro: IPR006671; Cyclin_N.
CC Pfam: PF00134; cyclin_1.
CC SMART: SM00384; cyclin_C; 1.
CC SMART: SM00385; CYCLIN; 2.
CC PROSITE: PS00292; CYCLINS; 1.
CC CYCLIN; Cell cycle; Cell division; Multigene family.
CC CONFLICT 25 DRV -> RPD (IN REF. 1).
CC SQUENCE 295 AA; 33482 MW; C777436B5C79635E CRC64;

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Query Match 3.6%; Score 11; DB 1; Length 295;
 Best Local Similarity 100.0%; Pred. No. 0.0078;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 101 LAMNYIDRPLS 111
DB 80 LAMNYIDRPLS 90

```

RESULT 8
 CGAL_XENIA STANDARD; PRT; 418 AA.
 AC P18606;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cyclin A1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=90360999; PubMed=2143983;
RA Minshull J., Colsteyn R., Hill C.S., Hunt T.;
RT "The A- and B-type cyclin associated cdc2 kinases in Xenopus turn on
RT and off at different times in the cell cycle."
RL EMBO J. 9:2865-2875(1990).
CC -1- FUNCTION: May be involved in the control of the cell cycle at the
CC G1/S (start) and G2/M (mitosis) transitions (By similarity).
CC -1- SUBUNIT: Interacts with the CDK2 and the CD2 protein kinases to
CC form a serine/threonine kinase holoenzyme complex. The cyclin
CC subunit imparts substrate specificity to the complex (By
CC similarity).
CC -1- DEVELOPMENTAL STAGE: Present in eggs and early embryos but cannot
CC be detected in late embryos.
CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin AB subfamily.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X53745; CAA37775.1; -
CC PIR: S11678; S11678.
CC HSSP: P30274; IVIN.
CC InterPro: IPR006670; Cyclin.
CC InterPro: IPR004367; Cyclin_Cterm.
CC InterPro: IPR006671; Cyclin_N.
CC Pfam: PF00134; cyclin_1.
CC SMART: PF00384; cyclin_C; 1.
CC SMART: SM00385; CYCLIN; 2.
CC PROSITE: PS00292; CYCLINS; 1.
CC CYCLIN; Cell cycle; Cell division; Mitosis.
CC SQUENCE 418 AA; 46772 MW; FEA0B7A1F0011B6A CRC64;

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Query Match 3.6%; Score 11; DB 1; Length 418;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 101 LAMNYIDRPLS 111
DB 220 LAMNYIDRPLS 230

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RESULT 9
 CGD2_RAT STANDARD; PRT; 288 AA.
 AC Q04837;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE G1/S-specific cyclin D2 (Vin-1 proto-oncogene).
 GN CCND2 OR VIN-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93275661; PubMed=8502486;
 RA Hanna Z., Jankowski M., Tremblay P., Jiang X.M., Milatovich A.,
 RA Franke U., Jolicoeur P.;
 RT "The Vin-1 gene, identified by provirus insertional mutagenesis, is
 RT the cyclin D2."
 RL Oncogene 8:1661-1666(1993).
 RN [2]

```

RP SEQUENCE FROM N.A.
RA MEDLINE=95011623; PubMed=7926809;
RA Hosokawa Y., Onga T., Nakashima K.;
RT "Induction of D2 and D3 cyclin-encoding genes during promotion of the
RT G1/S transition by prolactin in rat Nb2 cells.";
RL Gene 147:249-252(1994).
CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
CC (start) transition.
CC -1- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
CC impacts substrate specificity to the complex.
CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
CC -----
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CC -----
DR EMBL; L09752; AAA41010.1; -
DR EMBL; D16308; BAA03815.1; -
DR PIR; I58372; I58372.
DR PIR; JC4011; JC4011.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin C; 1.
DR SMART; SMO0385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLIN; 1.
KM CYCLIN, cell cycle, cell division; Multigene family; Proto-oncogene.
FT CONFLICT 68 E -> G (IN REF. 2).
FT CONFLICT 104 C -> V (IN REF. 2).
FT CONFLICT 232 T -> A (IN REF. 2).
SQ SEQUENCE 288 AA; 32826 MW; 4B522BFAE935FC1 CRC64;

Query Match 3.2%; Score 10; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 101 LAMNYLDRFL 110
Db 78 LAMNYLDRFL 87

RESULT 10
CGD2 HUMAN STANDARD; PRT; 289 AA.
AC P30279; O13955;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE G1/S-specific cyclin D2.
GN CCND2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92347851; PubMed=1386336;
RA Xiong Y., Menninger J., Beach D., Ward D.C.;
RT "Molecular cloning and chromosomal mapping of CCND genes encoding
RT human D-type cyclins.";
RL Genomics 13:575-584(1992).
[2]
RP SEQUENCE FROM N.A.
RA MEDLINE=93205384; PubMed=8455931;
RA Palmero I., Holder A., Sinclair A.J., Dickson C., Peters G.;
RT "Cyclins D1 and D2 are differentially expressed in human B-lymphoid
RT cell lines.";

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RL Oncogene 8:1049-1054(1993).
RN [3]
RP SEQUENCE FROM N.A.
RA Miyajima N.;
RT Submitted (MAR-1993) to the EMBL/GenBank/DBJ databases.
RL [4]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=22386257; PubMed=12477932;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Stausberg R.D., Collins P.S., Wagner L., Sherr C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan T., Max S.I., Wang J., Heife F.,
RA Datchenko L., Matsushita K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo W.F., Casavant J.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.D., Abramson R.D., Mallya S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[6]
RP SEQUENCE OF 1-240 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=92347850; PubMed=1386335;
RA Inaba T., Matsushime H., Valentine M., Rousset M.F., Sherr C.J.,
RA Look A.T.;
RT "Genomic organization, chromosomal localization, and independent
RT expression of human cyclin D genes.";
RL Genomics 13:565-574(1992).
CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
CC (start) transition.
CC -1- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
CC impacts substrate specificity to the complex.
CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M90813; AAA51926.1; -
DR EMBL; X68452; CAA48493.1; -
DR EMBL; D13639; BAA02802.1; -
DR EMBL; AF518005; AAM54041.1; -
DR EMBL; BC010958; AAT10958.1; -
DR EMBL; M88083; AAA51928.1; -
DR EMBL; M88080; AAA51928.1; JOINED.
DR EMBL; M88081; AAA51928.1; JOINED.
DR EMBL; M88082; AAA51928.1; JOINED.
DR PIR; A42822; A42822.
DR Genew; HGNC:1593; CCND2.
DR GK; P30279; -
DR MIM; 123833; -
DR InterPro; IPR006670; Cyclin.

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DR InterPro: IPR004367; Cyclin.Cterm.
DR InterPro: IPR006671; Cyclin_N.
DR Pfam: PF00134; cyclin_1.
DR SMART: SM00384; cyclin_C; 1.
DR SMART: SM00385; cyclin_C; 1.
DR PROSITE: PS00292; CYCLINS; 1.
DR Cyclin; Cell cycle; Cell division; Multigene family.
KW CONFLICT 166 167 KL -> NV (IN REF. 6).
FT CONFLICT 224 224 T -> H (IN REF. 6).
SQ SEQUENCE 289 AA; 33067 MW; E4ESFEF476D76D90 CRC64;

Query Match
Best Local Similarity 100.0%; Score 10; DB 1; Length 289;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANNYLDRFL 110
DB 79 LANNYLDRFL 88

RESULT 11
CGD2 MOUSE STANDARD; PRT; 289 AA.
AC P30280;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE G1/S-specific cyclin D2.
GN CCND2 OR CYL-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92196134; PubMed=1372445;
RA Kiyokawa H., Busquets X., Powell C.T., Ngo L., Rifkind R.A.,
RA Marks P.A.;
RT "Cloning of a D-type cyclin from murine erythroleukemia cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2444-2447(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91235305; PubMed=1827757;
RA Matsushima H., Roussel M.F., Ashmun R.A., Sherr C.J.;
RT "Colony-stimulating factor 1 regulates novel cyclins during the G1
RT phase of the cell cycle.";
RL Cell 65:701-713(1991).
CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
CC (start) transition.
CC -1- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
CC impacts substrate specificity to the complex.
CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
CC -----
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CC -----
CC EMBL: M83749; AAA37519.1; -.
CC EMBL: M86182; AAA37503.1; -.
CC PIR: A41984; A41984.
CC MGI: 88314; Ccnd2.
CC GO: 0000074; P:regulation of cell cycle; IMP.
DR InterPro: IPR006670; Cyclin.
DR InterPro: IPR004367; Cyclin.Cterm.
DR InterPro: IPR006671; Cyclin_N.
DR Pfam: PF00134; cyclin_1.
DR Pfam: PF02984; cyclin_C; 1.
DR SMART: SM00385; cyclin_C; 1.

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DR PROSITE: PS00292; CYCLINS; 1.
DR Cyclin; Cell cycle; Cell division; Multigene family.
KW CONFLICT 289 AA; 32897 MW; 58F32277DD1DA3D CRC64;
SQ SEQUENCE 289 AA; 32897 MW; 58F32277DD1DA3D CRC64;

Query Match
Best Local Similarity 100.0%; Score 10; DB 1; Length 289;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANNYLDRFL 110
DB 78 LANNYLDRFL 87

RESULT 12
CGD2 CHICK STANDARD; PRT; 291 AA.
AC P49706;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE G1/S-specific cyclin D2.
GN CCND2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96144302; PubMed=8566807;
RA Li H., Grenet J., Kidd V.J.;
RT "Structure and gene expression of avian cyclin D2.";
RL Gene 167:341-342(1995).
CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
CC (start) transition.
CC -1- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
CC impacts substrate specificity to the complex.
CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
CC -----
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CC -----
CC EMBL: U28980; AAA69655.1; -.
CC PIR: J04579; J04579.
DR InterPro: IPR006670; Cyclin.
DR InterPro: IPR004367; Cyclin.Cterm.
DR InterPro: IPR006671; Cyclin_N.
DR Pfam: PF00134; cyclin_1.
DR Pfam: PF02984; cyclin_C; 1.
DR SMART: SM00385; cyclin_C; 1.
DR PROSITE: PS00292; CYCLINS; 1.
DR Cyclin; Cell cycle; Cell division; Multigene family.
KW CONFLICT 291 AA; 33163 MW; 43A7E646AEAF3109 CRC64;
SQ SEQUENCE 291 AA; 33163 MW; 43A7E646AEAF3109 CRC64;

Query Match
Best Local Similarity 100.0%; Score 10; DB 1; Length 291;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANNYLDRFL 110
DB 79 LANNYLDRFL 88

RESULT 13
CGD2 XENLA STANDARD; PRT; 291 AA.
AC P53782;

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DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE G1/S-specific cyclin D2.
GN CCND2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RA SEQUENCE FROM N.A.
RA Cockrell M.J., Hunt T.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RP MEDLINE=97380591; PubMed=9237366;
RA Taleb F., Jesus C.;
RT "Xenopus cyclin D2: cloning and expression in oocytes and during
RT early development."
RL Biol. Cell 88:99-111(1996).
CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
CC (start) transition.
CC -1- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
CC imparts substrate specificity to the complex.
CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
CC -----
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CC -----
DR EMBL; X89456; CAA61665.1; -
DR EMBL; X83503; CAA58493.1; -
DR F01; S57925; S57925.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; Cyclin; 1.
DR Pfam; PF02988; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
KM Cyclin; Cell cycle; Cell division; Multigene family.
SQ SEQUENCE 291 AA; 32959 MW; 9A290F04F151B89 CRC64;

Query Match 2.9%; Score 9; DB 1; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 AMNYLDRFL 110
DB 80 AMNYLDRFL 88

RESULT 14
CGD3 ARATH STANDARD; PRT; 376 AA.
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclin delta-3.
GN CYCD3 OR AT4G34160 OR F28A23.80.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]

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RP SEQUENCE FROM N.A.
RP STRAIN=cv. Landsberg erecta; TISSUE=Seedling;
RC MEDLINE=95210930; PubMed=7696881;
RX Soni R., Carmichael J.P., Shah Z.H., Murray J.A.H.;
RA "A family of cyclin D homologs from plants differentially controlled
RT by growth regulators and containing the conserved retinoblastoma
RT protein interaction motif."
RL Plant Cell 7:85-103(1995).
RN [2]
RP REVISION TO 371.
RA Murray J.A.H.;
RA Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Scheller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Striekema W., Ertter K.-D., Terry N.,
RA Harris B., Anstorge W., Brandt P., Griwell L.A., Rieger M., Mueller M.,
RA Weichselgartner M., de Simone V., Obermayer B., Macne R., Mueller M.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hohnel J., Zimmermann W., Medler H., Ridley P.,
RA Langham S.-A., McCallagh B., Bilham L., Robben J.,
RA van der Schueren J., Grynoprez B., Chuang Y.-J., Vandenbusche F.,
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Kert R., Defoor E.,
RA Weltenssger T., Bothe G., Kampberger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Berninger S., Hempel S., Feldpausch M., Lambirth S., Van den Daele H.,
RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., Mclay K., Mayes R.,
RA Pettit A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Partmann B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Argirou A., Vitale D., Liguori R., Pirvadi E.,
RA Massenet O., Quigley F., Clabaud G., Muehlen A., Felber R.,
RA Schindl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chefor F., Cooke R., Berger C., Montfort A., Casacuberta E.,
RA Glibons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Frances P., Bielke C.,
RA Frisman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schütz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Lestrille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
RA Nelson J., Spith J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drome K., Cotton M., Jobu C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matere A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shondy N., Haegawa A., Hameed A., Lochi M., Johnson A.,
RA Chen E., Marra M.A., Martienssen R., McComble W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana."
RL Nature 402:769-777(1999).
CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; X83371; CAA58287.1; -

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DR EMBL: AL021961; CAA17556.1; -
 DR EMBL: AL161584; CAB80133.1; -
 DR PIR: T05420; T05420.
 DR InterPro: IPR006670; Cyclin.
 DR InterPro: IPR004367; Cyclin_Cterm.
 DR InterPro: IPR006671; Cyclin_N.
 DR Pfam: PF00134; cyclin; 1.
 DR Pfam: PF02984; cyclin; 1.
 DR SMART: SM00385; CYCLIN; 2.
 DR PROSITE: PS00292; CYCLINS; 1.
 DR Cyclin; Cell cycle; Cell division; Multigene family.
 KW CONFICT 288 C -> G (IN REF. 3).
 SQ SEQUENCE 376 AA; 42747 MW; FB8D5B5BC435FAC2 CRC64;

Query Match 2.9%; Score 9; DB 1; Length 376;
 Best Local Similarity 100.0%; Pred. No. 0.82;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 VACLSIAAK 136
 DB 137 VACLSIAAK 145

RESULT 15
 CGD3 HUMAN STANDARD; PRT; 292 AA.
 ID CGD3 HUMAN STANDARD; PRT; 292 AA.
 AC P30281; O96F49;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE GI/S-specific cyclin D3.
 GN CCND3.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A., AND VARIANT ALA-259.
 RX MEDLINE=92347851; PubMed=136336;
 RT "Molecular cloning and chromosomal mapping of CCND gene encoding
 human D-type cyclins.";
 RL Genomics 13:575-584 (1992).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93015922; PubMed=1383201;
 RT "Cloning and characterization of human cyclin D3, a CDNA closely
 related in sequence to the PRAD1/cyclin D1 proto-oncogene.";
 RL J. Biol. Chem. 267:20412-20415 (1992).
 [3]
 RP SEQUENCE FROM N.A., AND VARIANT ALA-259.
 RA Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Wittek L.A., Nickerson P.D.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RC TTSUB=lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Krausberg R.D., Collins F.S., Wagner C.H., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusik K., Farmer A.A., Rubin G.W., Hong L.,
 RA Sgajda M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Tohyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguella N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Heitton B., Ketterman W., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Smailus D.E.,
 RA Butlerfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [5]
 RP SEQUENCE OF 52-237 FROM N.A.
 RC TTSUB=Placenta;
 RX MEDLINE=92347850; PubMed=1386335;
 RA Inaba T., Matsushima H., Valentine M., Rousset M.F., Sherr C.J.,
 RA Look A.T.;
 RT "Genomic organization, chromosome localization, and independent
 expression of human cyclin D genes.";
 RL Genomics 13:565-574 (1992).
 CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
 (start) transition.
 CC -1- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
 a serine/threonine kinase holoenzyme complex. The cyclin subunit
 impacts substrate specificity to the complex.
 CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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 entities requires a license agreement (See <http://www.isb-sib.ch/annouce/>
 or send an email to license@isb-sib.ch).
 DR EMBL: M60814; AAA51927.1; -
 DR EMBL: M92287; AAA52137.1; -
 DR EMBL: AF517525; AAAS1826.1; -
 DR EMBL: BC011616; AAH11616.1; -
 DR EMBL: M80887; AAA51929.1; -
 DR EMBL: M80884; AAA51929.1; JOINED.
 DR EMBL: M80895; AAA51929.1; JOINED.
 DR EMBL: M80886; AAA51928.1; JOINED.
 DR PIR: B42822; B42822.
 DR Genew: HGNC:11585; CCND3.
 DR GK: P30281; -
 DR MM: 123834; -
 DR GO: GO:000074; P-regulation of cell cycle; TAS.
 DR InterPro: IPR006670; Cyclin.
 DR InterPro: IPR004367; Cyclin_Cterm.
 DR InterPro: IPR006671; Cyclin_N.
 DR Pfam: PF00134; cyclin; 1.
 DR Pfam: PF02984; cyclin; 1.
 DR SMART: SM00385; CYCLIN; 1.
 DR PROSITE: PS00292; CYCLINS; 1.
 KW Cyclin; Cell cycle; Cell division; Polymorphism; Multigene family.
 FT VARIANT 259 S -> A.
 SQ SEQUENCE 292 AA; 32519 MW; 16E7B1604FEB0029 CRC64;

Query Match 2.6%; Score 8; DB 1; Length 292;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDR 108
 DB 80 LAMNYLDR 87

Search completed: March 23, 2004, 16:47:15
 Job time : 37 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 16:43:48 ; Search time 45 Seconds

(without alignments)
2159.547 Million cell updates/sec

Title: US-09-530-209a-2

Sequence: 1 MAEENLESLCTESNVDE.....SACCFKTHDSSSYTHLS 308

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP viirus:*
16: SP bacteriaph:*
17: SP archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	308	100.0	308	10	Q9XFR7 arabidopsis
2	228	74.0	308	10	Q9XFR7 arabidopsis
3	171	55.5	308	10	Q8LGA1 arabidopsis
4	20	6.5	317	10	Q9LX96 arabidopsis
5	13	4.2	354	10	Q9ZRX9 arabidopsis
6	13	4.2	356	10	Q8SBC0 arabidopsis
7	13	4.2	382	10	Q8L6U0 arabidopsis
8	12	3.9	291	13	Q8AVQ4 xenopus lae
9	12	3.9	291	13	Q7ZYJ6 xenopus lae
10	12	3.6	191	11	Q8QFPA brachydanio
11	11	3.6	358	10	Q8S524 zea mays (m
12	11	3.2	156	11	Q9B819 mus musculu
13	10	3.2	190	10	Q57481 stizosectio
14	10	3.2	343	10	Q9SNV1 antirrhinum
15	10	3.2	350	10	Q7XAB6 euphorbia e
16	10	3.2	350	10	Q7XAB6 euphorbia e

17	10	3.2	355	10	Q7XAB7 euphorbia e
18	10	2.9	371	10	Q8AVB8 xenopus alb
19	9	2.9	153	13	P79919 xenopus lae
20	9	2.9	198	10	Q8S521 zea mays (m
21	9	2.9	315	10	Q8GVBO helianthus
22	9	2.9	321	10	Q8SZFE arabidopsis
23	9	2.9	330	10	Q9SNV2 antirrhinum
24	9	2.9	349	10	Q8Z678 chenopodium
25	9	2.9	372	10	P93103 chenopodium
26	9	2.9	390	10	Q8S522 zea mays (m
27	8	2.6	178	5	Q23641 caenorhabdi
28	8	2.6	232	17	Q97B27 thermoplasma
29	8	2.6	241	2	Q9ACH9 uncultured
30	8	2.6	241	2	Q9AE50 rhizobium 1
31	8	2.6	241	2	Q9AC12 uncultured
32	8	2.6	241	2	Q9AE49 rhizobium 1
33	8	2.6	241	2	Q9AC10 uncultured
34	8	2.6	241	2	Q9AE47 rhizobium 1
35	8	2.6	241	2	Q9AC14 uncultured
36	8	2.6	241	2	Q9ACH8 uncultured
37	8	2.6	263	10	Q22156 arabidopsis
38	8	2.6	300	17	Q28718 archaeoglob
39	8	2.6	302	5	Q964G0 strongyloce
40	8	2.6	302	10	Q9ZRO4 arabidopsis
41	8	2.6	306	5	Q9NEG4 leishmania
42	8	2.6	308	10	Q8LWP3 leishmania
43	8	2.6	328	16	Q9HZE3 pseudomonas
44	8	2.6	356	10	Q8LHA8 oryza sativ
45	8	2.6	357	10	Q8GVDS helianthus

ALIGNMENTS

RESULT 1
ID Q9XFR7 PRELIMINARY; PRT; 308 AA.
AC Q9XFR7;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE D-type cyclin.
GN CYCD4.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsie.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA de Veylder L., De Almeida Engler J., Bursens S., Maneyski A.,
RA Lescure B., Van Montagu M., Engler G., Inze D.;
RT "A new D-type cyclin of Arabidopsis thaliana expressed during lateral
RT root primordia formation."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL: AJ131636; CAB41347.1; -;
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0000910; P:cytokinesis; IEA.
DR GO: GO:0000740; P:regulation of cell cycle; IEA.
DR InterPro: IPR006670; Cyclin.
DR InterPro: IPR004367; Cyclin Cterm.
DR InterPro: IPR006671; Cyclin_N.
DR Pfam: PF00134; cyclin_1.
DR Pfam: PF02984; cyclin_1.
DR SMART: SM00385; CYCLIN; 1.
DR PROSITE: PS00292; CYCLINS; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 308 AA; 34687 MW; 591ADA3361DD63D CRC64;
Query Match 100.0%; Score 308; DB 10; Length 308;
Best Local Similarity 100.0%; Pred. No. 1.7e-297; Indels 0; Gaps 0;
Matches 308; Conservative 0; Mismatches 0;

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QY 1 MAENNELSLCTESNVDEGMIVDETPRISIPQWFGSSESEETIMENEKEXCHLPS 60
DB 1 MAENNELSLCTESNVDEGMIVDETPRISIPQWFGSSESEETIMENEKEXCHLPS 60
QY 61 DDYIKRLRSGDDLNVGRDALNMWIKACEVHGFPLCFLANNYLDRLFSVHDLPSGKG 120
DB 61 DDYIKRLRSGDDLNVGRDALNMWIKACEVHGFPLCFLANNYLDRLFSVHDLPSGKG 120
QY 121 WIQLAVACLSIAAKIEETEVPMILIDVGDPOQVFEAKSVQRMELLVANKMLRLAI 180
DB 121 WIQLAVACLSIAAKIEETEVPMILIDVGDPOQVFEAKSVQRMELLVANKMLRLAI 180
QY 181 TPQSYIRYFLRKMSKCDQEPSNTLISRSQVIASTTKGIDPLEFRPSEAAAVALSVSGE 240
DB 181 TPQSYIRYFLRKMSKCDQEPSNTLISRSQVIASTTKGIDPLEFRPSEAAAVALSVSGE 240
QY 241 LQVHFNSSPSPFLSLQKERYKIGEMIESGSDSCQTPNGVLEVSACCFSPKTHDS 300
DB 241 LQVHFNSSPSPFLSLQKERYKIGEMIESGSDSCQTPNGVLEVSACCFSPKTHDS 300
QY 301 SSSYTHLS 308
DB 301 SSSYTHLS 308

RESULT 2
Q9FKP7 PRELIMINARY; PRT; 308 AA.
AC Q9FKP7;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE D-type cyclin.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Feldmann K.;
RA "Full-length cDNA from Arabidopsis thaliana."
RT Submitted (MAR-2002) to the EMBL/GenBank/DBS databases.
RL -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
CC EMBL; AY084386; AAM60963.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cyclokinesis; IEA.
DR GO; GO:000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR SMART; SM00385; CYCLIN_C; 1.
DR SMART; SM00385; CYCLIN_N; 1.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 308 AA; 34715 MM; 96FD929C868DD62F CRC64;

Query Match 74.0%; Score 228; DB 10; Length 308;
Best Local Similarity 100.0%; Pred. No. 6e-218;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAENNELSLCTESNVDEGMIVDETPRISIPQWFGSSESEETIMENEKEXCHLPS 60
DB 1 MAENNELSLCTESNVDEGMIVDETPRISIPQWFGSSESEETIMENEKEXCHLPS 60
QY 61 DDYIKRLRSGDDLNVGRDALNMWIKACEVHGFPLCFLANNYLDRLFSVHDLPSGKG 120
DB 61 DDYIKRLRSGDDLNVGRDALNMWIKACEVHGFPLCFLANNYLDRLFSVHDLPSGKG 120

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DB 61 DDYIKRLRSGDDLNVGRDALNMWIKACEVHGFPLCFLANNYLDRLFSVHDLPSGKG 120
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DB 121 WIQLAVACLSIAAKIEETEVPMILIDVGDPOQVFEAKSVQRMELLVANKMLRLAI 180
QY 181 TPQSYIRYFLRKMSKCDQEPSNTLISRSQVIASTTKGIDPLEFRPSE 228
DB 181 TPQSYIRYFLRKMSKCDQEPSNTLISRSQVIASTTKGIDPLEFRPSE 228

RESULT 3
Q9LX96 PRELIMINARY; PRT; 308 AA.
AC Q9LX96;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE D-type cyclin.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volkovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation."
RL Genome Biol. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana."
RT Submitted (MAR-2002) to the EMBL/GenBank/DBS databases.
RL -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
CC EMBL; AY084386; AAM60963.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cyclokinesis; IEA.
DR GO; GO:000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR SMART; SM00385; CYCLIN_C; 1.
DR SMART; SM00385; CYCLIN_N; 1.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 308 AA; 34788 MM; EB077DA1868DC42 CRC64;

Query Match 55.5%; Score 171; DB 10; Length 308;
Best Local Similarity 100.0%; Pred. No. 2.9e-161;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAENNELSLCTESNVDEGMIVDETPRISIPQWFGSSESEETIMENEKEXCHLPS 60
QY 61 DDYIKRLRSGDDLNVGRDALNMWIKACEVHGFPLCFLANNYLDRLFSVHDLPSGKG 120
DB 61 DDYIKRLRSGDDLNVGRDALNMWIKACEVHGFPLCFLANNYLDRLFSVHDLPSGKG 120
QY 121 WIQLAVACLSIAAKIEETEVPMILIDVGDPOQVFEAKSVQRMELLVANKMLRLAI 171
DB 121 WIQLAVACLSIAAKIEETEVPMILIDVGDPOQVFEAKSVQRMELLVANKMLRLAI 171

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AC Q9LX96;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cyclin protein-like.
GN F12B17.210.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL: A135395; CAB89399.1; -.
DR PIR: T49995; T49995.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0000910; P:cytokinesis; IEA.
DR GO: GO:000074; P:regulation of cell cycle; IEA.
DR InterPro: IPR006670; Cyclin.
DR InterPro: IPR004367; Cyclin_Cterm.
DR Pfam: PF00134; cyclin; 1.
DR Pfam: PF02984; cyclin_C; 1.
DR SMART: SM00385; CYCLIN; 1.
DR PROSITE: PS00292; CYCLIN; 1.
DR Cell cycle; Cell division; Cyclin.
KW SEQUENCE 317 AA; 35910 MW; 07616F8480927711 CRC64;
SQ
Query Match 6.5%; Score 20; DB 10; Length 317;
Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 CLAMNYLDRPLSVHDPGSK 119
DB 91 CLAMNYLDRPLSVHDPGSK 110

RESULT 5
Q9ZRX9
ID Q9ZRX9 PRELIMINARY; PRT; 354 AA.
AC Q9ZRX9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cyclin D2.1 protein.
GN C1CD2.1.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE:90937070; PubMed:980377;
RA Sorrell D.A., Combettes B., Chaubet-Gigot N., Gigot C., Murray J.A.H.;
RT "Distinct Cyclin D Genes Show Mitotic Accumulation or Constant Levels
RT of Transcripts in Tobacco Bright Yellow-2 Cells.";
RL Plant Physiol. 119:343-351(1999).
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL: A011892; CA09852.1; -.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0000910; P:cytokinesis; IEA.
DR GO: GO:000074; P:regulation of cell cycle; IEA.
DR InterPro: IPR006670; Cyclin.
DR InterPro: IPR004367; Cyclin_Cterm.
DR InterPro: IPR006671; Cyclin_N.

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DR Pfam: PF00134; cyclin; 1.
DR Pfam: PF02984; cyclin_C; 1.
DR SMART: SM00385; CYCLIN; 1.
DR PROSITE: PS00292; CYCLIN; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 354 AA; 39714 MW; 18363A0E76E89BF CRC64;

Query Match 4.2%; Score 13; DB 10; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QLIYVACLSIAK 136
DB 142 QLIYVACLSIAK 154

RESULT 6
Q8SBG0
ID Q8SBG0 PRELIMINARY; PRT; 356 AA.
AC Q8SBG0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cyclin.
GN OSCYCD.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipondare;
RA Nakashima M., Neogi P.B., Okano E., Hashimoto J., Sasaki T.,
RA Ichikawa H.;
RT "Nucleotide sequence of a cDNA encoding a D-type cyclin from cell
RT suspension culture of rice.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL: AB080248; BAB85522.1; -.
DR Gramene: Q8SBG0; -.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0000910; P:cytokinesis; IEA.
DR GO: GO:000074; P:regulation of cell cycle; IEA.
DR InterPro: IPR006670; Cyclin.
DR InterPro: IPR004367; Cyclin_Cterm.
DR InterPro: IPR006671; Cyclin_N.
DR Pfam: PF00134; cyclin; 1.
DR Pfam: PF02984; cyclin_C; 1.
DR SMART: SM00385; CYCLIN; 1.
DR PROSITE: PS00292; CYCLIN; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 356 AA; 38937 MW; 502AF4EB9CE8BC6A CRC64;

Query Match 4.2%; Score 13; DB 10; Length 356;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QLIYVACLSIAK 136
DB 149 QLIYVACLSIAK 161

RESULT 7
Q8L6U0
ID Q8L6U0 PRELIMINARY; PRT; 382 AA.
AC Q8L6U0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cyclin D2.
GN CYCD2.
OS Daucus carota (Carrot).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Campanulid; Apiales; Apiales; Apiales; Apiales; Apiales; Apiales;
OC Daucus.
OX NCBI_TaxID=4039;
RN [1]
RP SEQUENCE FROM N.A.
RA Eun C.H., Ko S.M., Matsubayashi Y., Sakagami Y., Kamada H.;
RT "The effect of the peptidyl growth factor, phytoosulfolone- $\alpha$ , on
RT the cell cycle progression in carrot non-embryogenic cells."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AF496740; C:43141.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cyclohexis; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
KM Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 382 AA; 43354 MW; 79768528D809170 CRC64;

Query Match 4.2%; Score 13; DB 10; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QLVAVCLSLAAK 136
DB 141 QLVAVCLSLAAK 153

RESULT 8
Q8AVQ4 PRELIMINARY; PRT; 291 AA.
AC Q8AVQ4;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Similar to cyclin D1 (PRAD1: parathyroid adenomatosis 1).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Embryo;
RC Klein S.; Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041525; AAH41525.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
KM Cyclin.
SQ SEQUENCE 291 AA; 33052 MW; 55316D5236F9E081 CRC64;

Query Match 3.9%; Score 12; DB 13; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRPLSV 112
DB 78 LAMNYLDRPLSV 89

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RESULT 9
Q7ZYU6 PRELIMINARY; PRT; 291 AA.
AC Q7ZYU6;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Embryo;
RC Klein S.; Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC043758; AAH43758.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
DR PROSITE; PS00038; HLH_1; 1.
KM Hypothetical protein.
SQ SEQUENCE 291 AA; 33005 MW; 6678C2C9EACF9178 CRC64;

Query Match 3.9%; Score 12; DB 13; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRPLSV 112
DB 78 LAMNYLDRPLSV 89

RESULT 10
Q8QFP4 PRELIMINARY; PRT; 291 AA.
AC Q8QFP4;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cyclin D1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Mature ovary;
RC Bauer M.P.; Goetz F.W.;
RL "Isolation of Cyclin D1 from the Zebrafish."
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AF365874; AA00355.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cyclohexis; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR006671; Cyclin_Cterm.
DR InterPro; IPR004367; Cyclin_N.
DR InterPro; IPR001092; HLH_basic.

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DR Pfam: PF00134; cyclin_1.
 DR Pfam: PF02984; cyclin_C; 1.
 DR SMART; SM00385; CYCLIN; 1.
 DR PROSITE; PS00292; CYCLIN; 1.
 DR PROSITE; PS00038; HLH 1; 1.
 KW Cell cycle; Cell division; Cyclin.
 SQ SEQUENCE 291 AA; 33080 MW; 7848FCCF2482E8 CRC64;

Query Match 3.6%; Score 11; DB 11; Length 291;
 Best Local Similarity 100.0%; Pred. No. 0.0035;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANVYLDRLSV 112
 DB 80 LANVYLDRLSV 91

RESULT 11
 O99NB4 PRELIMINARY; PRT; 191 AA.

AC O99NB4; 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Cyclin D1 (Fragment)
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCB1_TaxID=10116;

RN [1] SEQUENCE FROM N.A.

RC STRAIN=WiStar;
 RA Morinuchi A.; Ido A.; Tsubouchi H.;
 RT "Characterization of rat cyclin D1 5' flanking region."
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.

DR EMBL; AB042564; BAB4033.1; -

DR HSSP; P30274; 1VIN.

DR GO; GO:0005634; Cytocytosol; IEA.

DR GO; GO:0000910; P:cytokinesis; IEA.

DR GO; GO:0000074; P:regulation of cell cycle; IEA.

DR InterPro; IPR006670; Cyclin.

DR InterPro; IPR004367; Cyclin_Cterm.

DR InterPro; IPR006671; Cyclin_N.

DR Pfam; PF00134; cyclin; 1.

DR Pfam; PF02984; cyclin_C; 1.

DR SMART; SM00385; CYCLIN; 1.

DR PROSITE; PS00292; CYCLIN; 1.

DR PROSITE; PS00038; HLH 1; 1.

KW Cell cycle; Cell division; Cyclin.

KW NON TER

ST SEQUENCE 191 AA; 22203 MW; AA97B60F32DEDE CRC64;

Query Match 3.6%; Score 11; DB 11; Length 191;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANVYLDRLSV 111
 DB 80 LANVYLDRLSV 90

RESULT 12
 O85524 PRELIMINARY; PRT; 358 AA.

AC O85524; 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE D-type cyclin.

GN CYCD2.

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 NC NCB1_TaxID=4577;

RN [1] SEQUENCE FROM N.A.

RC STRAIN=cv. Mo17;

RA Tao Y.; Lowe K.; Gregory C.; Coughlan S.J.; Gordon-Kamm W.J.;

RT "Isolation of a family of D-type cyclins from maize that show

conserved and unique characteristics."

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.

DR EMBL; AF351189; AAL83926.1; -

DR GO; GO:0005634; Cytocytosol; IEA.

DR GO; GO:0000910; P:cytokinesis; IEA.

DR GO; GO:0000074; P:regulation of cell cycle; IEA.

DR InterPro; IPR006670; Cyclin.

DR InterPro; IPR004367; Cyclin_Cterm.

DR InterPro; IPR006671; Cyclin_N.

DR Pfam; PF00134; cyclin; 1.

DR Pfam; PF02984; cyclin_C; 1.

DR SMART; SM00385; CYCLIN; 1.

DR PROSITE; PS00292; CYCLIN; 1.

KW Cell cycle; Cell division; Cyclin.

SQ SEQUENCE 358 AA; 38836 MW; D25B39B7D640837 CRC64;

Query Match 3.6%; Score 11; DB 10; Length 358;
 Best Local Similarity 100.0%; Pred. No. 0.041;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QILAVACLSLA 134
 DB 148 QILAVACLSLA 158

RESULT 13
 O99BL9 PRELIMINARY; PRT; 156 AA.

AC O99BL9; 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Cyclin D2.

GN CCND2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NC NCB1_TaxID=10090;

RN [1] SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Pancreas;

RA Kawai J.; Shinagawa A.; Shibata K.; Yoshino M.; Itoh M.; Ishii Y.;

RA Arakawa T.; Hara A.; Fukunishi Y.; Kono H.; Adachi S.; Yamada I.;

RA Aizawa K.; Izawa M.; Nishi K.; Kiyosawa H.; Kondo S.; Yamada I.;

RA Saio T.; Okazaki Y.; Gojobori T.; Bono H.; Kasukawa T.; Saio R.;

RA Kadoya K.; Macsuda H.A.; Ashburner M.; Batalov S.; Caavaant T.;

RA Fleischmann W.; Gaasterland T.; Gissi C.; King B.; Kochiwa H.;

RA Kuehl P.; Lewis S.; Matsuo Y.; Nikaide I.; Pesole G.; Quackenbush J.;

RA Schriml L.M.; Staubli F.; Suzuki R.; Tomita M.; Wagner L.; Mashio T.;

RA Sakai K.; Okido T.; Furuno M.; Aono H.; Baldarelli R.; Barsh G.;

RA Blake J.; Boffelli D.; Bojunga N.; Carninci P.; de Bonaldo M.F.;

RA Brownstein M.C.; Bult C.; Fletcher C.; Fujita M.; Gariboldi M.;

RA Gustinich S.; Hill D.; Hofmann M.; Hume D.A.; Kamya M.; Lee N.H.;

RA Lyons P.; Marchionni L.; Mashima J.; Mazzarelli J.; Mombarts P.;

RA Nordone P.; Ring B.; Ringwald M.; Rodriguez I.; Sakamoto N.;

RA Sasaki H.; Sato K.; Schoenbach C.; Seya T.; Shibata Y.; Storch K.-F.;

RA Suzuki H.; Toyokawa K.; Wang K.H.; Weltz C.; Whitaker C.; Williams L.;

RA Wyszynski B.; Yoshida K.; Hasegawa Y.; Kawai H.; Kohseki S.;

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection."

RL Nature 409:685-690(2001).

CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.

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DR EMBL; AJ007904; BAB25338.1; -.
DR HSSP; P38274; 1VIN.
DR MGD; MG188314; Cond2.
DR GO; GO:0000074; P:regulation of cell cycle; IMP.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
DR Cell cycle; Cell division; Cyclin.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 156 AA; 18080 MW; C0215E724C6B9CFE CRC64;

Query Match 3.2%; Score 10; DB 11; Length 156;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDREFL 110
DB 78 LAMNYLDREFL 87

RESULT 14
057481 PRELIMINARY; PRT; 190 AA.
AC 057481;
DT 01-JUN-1998 (TRENBLREL. 06, Created)
DT 01-JUN-1998 (TRENBLREL. 06, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Cyclin D (Fragment).
OS Stizostedion vitreum.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Percidae; Stizostedion.
OC NCBI_TaxID=57868;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98440539; Pubmed=9765420;
RA Lapiere L.A., Casey J.W., Holtschu D.L.;
RT "Walleye retroviruses associated with skin tumors and hyperplasias
RT encode cyclin D homologs."
RL J. Virol. 72:8765-8771(1998).
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AF037570; AAC68476.1; -.
DR HSSP; P30274; 1VIN.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR Cell cycle; Cell division; Cyclin.
KW NON TER 1
FT NON TER 1
SQ SEQUENCE 190 AA; 21445 MW; 5EB1B9BA969C01BC CRC64;

Query Match 3.2%; Score 10; DB 13; Length 190;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDREFL 110
DB 18 LAMNYLDREFL 27

RESULT 15
Q9SNV1 PRELIMINARY; PRT; 343 AA.
AC Q9SNV1;
DT 01-MAY-2000 (TRENBLREL. 13, Created)

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DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Cyclin D3a (Fragment).
GN CYCD3A.
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Plantaginaceae; Antirrhineae; Antirrhinum.
OC NCBI_TaxID=4151;
RN [1]
RP SEQUENCE FROM N.A.
RA Gaudin V., Lunnese P., Fobert P., Towers M., Riou-Khamlich C.,
RA Murray J., Coen E., Doonan J.H.;
RT "The expression of D-cyclin genes define distinct developmental zones
RT in Antirrhinum apical meristems and is locally regulated by the
RT cycloidea gene."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AJ250397; CAB61222.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
DR Cell cycle; Cell division; Cyclin.
KW NON TER 343
FT NON TER 343
SQ SEQUENCE 343 AA; 39254 MW; 128210AB2FC6E2C6 CRC64;

Query Match 3.2%; Score 10; DB 10; Length 343;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 AVACLSIAAK 136
DB 136 AVACLSIAAK 145

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Search completed: March 23, 2004, 16:48:14
Job time : 65 secs